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ALIGNMENTS

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-95379848; PubMed-7651420;
MEDLINE-95379848; PubMed-7651420;
Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-r., ____
Zhu X., Mancini M.A., Chang K.-H.,
Jones D., Yang-Feng T.L., Lee W.-H.;
Jones D., Yang-Feng T.L., Lee W.-H.;
"Characterization of a novel 350-kilodalton nuclear phosphoprotein
that is specifically involved in mitotic-phase progression.";
that is specifically involved in mitotic-phase progression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
SEQUENCE OF 2194-3210 FROM N.A.
MEDLINE-95336446; PubMed-7612011;
Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., J
"A novel cell-cycle-dependent 350-kDa nuclear protein:
"A novel cell-cycle-dependent localization.";
domain sufficient for nuclear localization.";
domain sufficient Res. Commun. 212:220-228(1995).
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                          CHARACTERIZATION.

MEDLINE=98437347; PubMed=9763420;
Chan G.K.T., Schaar B.T., Yen T.J.;
Chan G.K.T., Schaar B.T., Yen T.J.;
Chan G.K.T., Schaar B.T., Yen T.J.;

"Characterization of the kinetochore binding domain of CENP-E re
Interactions with the kinetochore proteins CENP-F and hBUBRI.";

J. Cell Biol. 143:49-63(1998).

-!- FUNCTION: PROBABLY REQUIRED FOR KINETOCHORE FUNCTION, INVOLV.

CHROMOSOME SEGREGATION DURING MITOSIS. INTERACTS WITH
RETINOBLASTOMA PROTEIN (RB), CENP-E AND BUBRI.

-!- SUBUNIT: HOMO- OR HETERODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95370296; pubMed=7642639; Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., Lee W.-H.; The C terminus of mitosin is essential for its nuclear localization. centromere/kinetochore targeting, and dimerization."; J. Biol. Chem. 270:19545-19550(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95348175; PubMed=7542657;
Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;
"CENP-F is a protein of the nuclear matrix that assembles onto kinetochores at late G2 and is rapidly degraded after mitosis.";
J. Cell Biol. 130:507-518(1995).
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TISSUE=Breast carcinoma;
MEDLINE=95348175; PubMed
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   <del>:</del> :
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   SUBCELLULAR LOCATION:
NUCLEAR MATRIX (BUT NOT IN THE NUCLEOLUS),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REORGANIZATION TO THE KINETOCHORE/CENTROMERE (CORONAL THE OUTER PLATE) AND THE SPINDLE DURING MITOSIS.

DEVELOPMENTAL STAGE: GRADUALLY ACCUMULATES DURING THE
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                                                                     EKEDLTNELQKEQERISELEIINSSFENILQEKEQEKVQMKEKS
                                                                                          KLKTLNTELDQ-----AKLEL--RSAQKDLQSADQEITSLRKKS
                                                                                                                 LLKGRVENLERELEIARTNQEHAALEAENSKGEVETLKAKIEGMTQSLRGLELDVVTIRS
                                                                                                                                        ----VEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRS
                                                                                                                                                               AALCGDQEIMKATEQSLDPPIEEEHQLRNSIEKLRARLEADEKKQLCVLQQLKESEHHAD
                                                                                                                                                                                      STL---KKQMKFLEQRQD----ETKQAREEAHRLKCKMKTMEQIELLLQSQRSE-----
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L -> Q (IN REF. 3).
D -> N (IN REF. 2).
ELWERVAALHNDQEACK -> SSMREWQ (IN REF. 3).
(IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEAR LOCALIZATION S:

T -> A (IN REF. 2).

L -> Q (IN REF. 2).

G -> D (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 2).

V -> A (IN REF. 2).

V -> L (IN REF. 2).

LER -> DG (IN REF. 3).
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01-OCT-1996 (Rel. 34
Hypothetical 222.8 k
SPAC1F3.06C.
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain,
type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use of the profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use by non-profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as its content use of the profit institutions as long as i
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                            SEQUENCE FROM N.A. Ohara M., Ishiguro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1566
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                                                                                                                                 Mammalia; Eutheria;
Bovidae; Bovinae; Bo
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea
                                                                                                                                                                                                                                                                                                                                                                                      027991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical SEQUENCE 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                                          Bos taurus (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                                   MYHA_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; Z70690; CAA94624.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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1957 AA;
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34, Last sequence update)
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8 kDa protein ClF3.06C in ch
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Shinagawa M.;
nyosin heavy chain
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Bos taurus

nonmuscle

myosin

B mRNA,

complete cds.";

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Best Local :
                                                                                                                                                                     Matches
                                                                                                                                                                                                                                       NP_BIND
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   SMART;
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PTODOM: PD000355; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION CAPPING (BY SIMILARITY).

SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPT CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myosin heavy chain in ...
J. Biol. Chem. 270:14533-14540(1995).
-I- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE
-I-- THE TOWNS AND SPECIALIZED FUNCTIONS SUCH AS SEC
 1198
                                                       1138
                                                                                                              1078
                                                                                                                                                                                                                                                                 Coiled coil; Alkylation; Multigene family.

DOMAIN

1 785

WYOSIN HEAD-L.

DOMAIN
786

B15

COILED COIL ()

NP_BIND
178
185

ATP (POTENTIA)

MOD_RES
701
701

ALKYLATION (S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB022023; BAA36494.;
EMBL; U15716; AAA87715.1;
HSSP; P08799; 1LVK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-1999)
[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 204-302
                                                                                                                                                                                                                                                                                                                                                    Myosin; ATP-binding; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Neuronal cell expression of inserted isoforms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Itoh K., Adelstein R.S
                           88
                                                                                  39
                                                                                                                                      European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
RORHATALEELSEQLEQAKRFKANLEKNKOGLETDNKELACEVKVLOQVKAESEHKRKKL
                                                  EKQKRDLSEELEALKTELEDTLDTTAAQQELRTKREQEVAELKKALEEETKSHEAQIQDM
                                                                               IDELKIQVAKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFESEKASRNKA 1137
                          PF00612; IQ; 1
                                                                                                                                                                                                                                                                                                                                                                                SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                               SM00015;
                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           o; IPRO00048; IQ.
i; IPRO04009; Myosin_N.
i; IPRO02228; Myosin_tail.
i; IPR0022017; Spectrin.
i; IPR001609; myosin_head.
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                                                                                                                                                                                                                                                                                                                                                                                                IQ; 1.
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21.4%;
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                                                                                                                                                                                                                    IQ.

COILED COIL (POTENTIAL).

ATP (POTENTIAL).

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

77 MW; 6144354451C0£790 CRC64;
                                                                                                                                                                     58;
                                                                                                                                                                               Score 169; DB 1; Length 1976; Pred. No. 0.027;
                                                                                                                                                                                                                                                                                                                           MYOSIN HEAD-LIKE
                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no rest
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RESULT 4
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                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not remove entities requires a license agreement (so or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collable between the Swiss Institute of Bioinformatics and the EMBL outsi the European Bioinformatics Institute. There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Seq. 7:71-82(1997).
-!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN SPERMATOGENESIS AND/OR TESTIS DEVELOPMENT. PROBABLY IDENTICAL WITH THE SEROLOGICALLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Golgin-160 (Male-enhanced antigen-2) GOLGA3 OR MEA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1374 TDTKKKVDD 1382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoantigen."
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"Cloning and molecular characterization of cDNA encoding a "Cloning and molecular characterization of encoding a putative family of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           male-enhanced antigen-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CD-1; TISS
MEDLINE=97217683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G160_MOUSE
                                                                                                                                                                                                     Spermatogenesis; Developmental protein.
DOMAIN 201 204 POLY-ALA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                  MGD; MGI:96958; Golga3.
                                                                                                                                                                                                                                                               EMBL; D78270; BAA19612.1;
                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                          DETECTABLE MALE ANTIGEN (SDM).

TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS.
FOUND IN SPERMATIDS DURING SPERMATOGENESIS. NO
LEYDIG CELLS, SPERMATOGONIA, OR SPERMATOCYTES.
SIMILARITY: HIGH, TO HUMAN GOLGIN-160.
CAUTION: IT IS UNCERTAIN WHETHER MET-1, MET-19
                                                                                                                                                                                                                                                                                                                                                                                                                 INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TSLRKKSDD
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DLAVKSNQVEHLQQE-----TATLRKQMQKVKEQFVQQKVMVEAYRRDATSKDQLINE
                                                                                    DLAQEEENVLDA-EFLKNE------LDSVKAQLSQKDREKR------DSQAIIDTLRD
                           TLEERNATVESLQNALNKAEMLCSTLKKQM-----KFLEQ------RQDET------KQ
                                                        ELQREADSREDAIHFLQNEKIVLEVALQSAKSDKEELDRGARRLEEDTEETSGLLEQLRQ
                                                                                                                 69; Conservative
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1325 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=9063644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35, Created)
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                                                                                                                                                                                                                                                                                                                        institutions as long as its content atement is not removed. Usage by an
                                                                                                                               15.7%;
                                                                                                                                                                                         149880 MW;
                                                                                                                  50;
                                                                                                                 Score 168.5; DE Pred. No. 0.019; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                         3230636962C687B0
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(MEA-2).
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                                                                                                                                                                                         CRC64;
                                                                                                                                              Length 1325;
                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XCPE_XENLA
P50533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         condensation in vitro.";
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                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                     NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "A heterodimeric coiled-coil protein required for mitotic chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hirano T., Mitchison T.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=95042742; PubMed=7954811;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MITOTIC CHROMOSOMES.
SUBBURI: ASSOCIATES WITH XCAP-C PROBABLY AS HETERODIMER.
SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN
MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND
MITOTIC EXTRACTS, THE STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.
FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.
DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS
FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: REQUIRED FOR
QKEMKTKHKAYENAVSILSRRLQEALASKEATDAELNQLRAQSTGGSSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLELRSAQKDLQSA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79:449-458(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RDEMETHLQSLKFDKEQMTALTEANETLKKQTEELQQEAKKATTEQKQKMKRLGSDLTSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U13674; AAA64680.1;
P07751; 1AJ3.
                                                                                                                                                                                                                                                                                                                                                                                                 PF02483; SMC_C;
PF02463; SMC_N;
                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-profit institu
                                                                                                                                                                                                                                                                                                                                                                         ATP-binding;
                                                                               15.6%;
nilarity 24.6%;
Conservative 4
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356
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513
1032
1121
3 AA; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Latement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                           Coiled
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                                                                                  45;
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                                                                                                                                                                                                              ed coil; Nuclear protein.
ATP (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
ALA/ASP-RICH (DA-BOX).
ALA/ASD-0123DD0027DF309 CRC64;
                                                                               Score 167.5;
Pred. No. 0.02
45; Mismatches
                                                                                                                                                                                                                       ¥.
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                                                                                                        .02;
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RESULT 6
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01-JUN-1994
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                           Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                            use by non-profit institutions as long as modified and this statement is not removed. Use this requires a license agreement (See htter
                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; MuscEphydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MYSN_DROME Q99323;
                                                                                                                InterPro; IPR002928; InterPro; IPR001609; Pfam; PF00612; IQ; 1.
                                                                                                                                                              FlyBase; FBgn0005634; InterPro; IPR000048; I
                                                                                                                                                                                                   PIR; A36014; A36014.
PIR; B36014; B36014.
                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Embryo;
MEDLINE=90349606; PubMed=2117279;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin
                                                                                                                                                                                                                            EMBL; M35012; AAA28713.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly)
                                                                                                                                                     InterPro; IPR004009;
                                                                                                                                                                                        HSSP; P08799; 1MMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
chain, non-muscle (Zipper protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----TTYKQQIETVDEAMKAYQEQADSMASEVSKNKEAVKKAQDELAKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                            Myosin_tail.myosin_head.
                                                                                                                                                     Myosin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218
                                                                                                                                                                                                                                                            (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein) (Myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
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tail and differential
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PROSITE; Psource Prosin; Alternative

rnative splicing; Co
Calmodulin-binding.

Coiled

coil;

Actin-binding

SMART;

; SM00015; IQ; 1.; SM00242; MYSC; TE; PS50096; IQ;

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TOOL-WILL OF THE PROPERTY OF T
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NP_BIND
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USO1_YEAST
P25386;
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1992 (Rel. 22, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
Intracellular protein transport protein USO1.
USO1 OR INT1 OR YDL058W.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                   Bai Y., Symington L.S.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: REQUIRED FOR PROTEIN TRANSPORT FROM THE E
                                                                                                                                                                                                                                                                                                      MEDLINE-91185402; PubMed-2010462; Nakajima H., Hirata A., Ogawa Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1492
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                                                                                SEQUENCE OF 1-8 FROM N.A.
                                                                                                                        Submitted (FEB-1993)
                                                                                                                                           Kendrick K.E
                                                                                                                                                                                   SEQUENCE OF
                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                    STRAIN-X2180-1A;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                            Hostetter M.K.,
                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                "A cytoskeleton-related gene, uso1,
                                                                                                                                                                                                                                                                                       Yamasaki M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214
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    COMPLEX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                          transport in Saccharomyces Biol. 113:245-260(1991).
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                                                                                                                                                                Herman
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859
2017
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2017
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COILED COIL (POTENTIAL).
ATP.
25 KDA/50 KDA JUNCTION.
50 KDA/20 KDA JUNCTION.
ACTIN-BINDING.
REACTIVE SULFHYDRYL/ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLOBULAR TAILPIECE.
MISSING (IN SHORT ISOFORM)
MW; 73E3CB02BA8F2528 CRC64
                                                                                                                      EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 166; DB Pred. No. 0.04; Mismatches
                                                                                                                                                              Bendel C.M., McClellan M.,
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ALPHA-HELICAL TAILPIECE (LMM).
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cerevisiae.";
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sequence update) annotation updat

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Dictyostelium discoideum (Slime mold)

Mycetozoa; Dictyosteliida;

Dictyostelium

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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
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                                             184 LNTELDQAKLELRSAQKDLQSADQEITSLRKKSDD
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BL; L03188; AAB600143.1; -.
BL; U53668; AAB66659.1; -.
R; A38455; A38455.
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D; P80220; IDIP.
D; S0002216; USO1.
D; S0002216; USO1.
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ER AND THE GOLGI COMPLEX.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, COMPOSED OF AN HEPTAPEPTIDE REPEAT PATTERN CHARACTERISTIC OF ALPHA-HELICAL COILED COILS. MAY FORM FILAMENTOUS STRUCTURES IN THE CELL.

SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
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SGSELETVKQELNNAQEKIRINAEENTVLKSKLED
                                                                                               ETIRKSDEKLEQ-----SKKSAEEDIKNLQHEKSDLISRINESEKDIEELKSKLRIEAK
                                                                                                                                                                                          LRAAQESKAKVEEGLKKLEEESSKEKAELEKSKEM-----MKKLESTIESNETELKSSM
                                                                                                                                          RDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRL---KKDLVSSRSKLK---T
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E -> K (IN REF. 2).
V -> I (IN REF. 2).
I -> V (IN REF. 2).
N -> S (IN REF. 2).
G -> S (IN REF. 2).
I -> V (IN REF. 2).
I -> V (IN REF. 2).
D -> DEEDDEE (IN REF. 2).
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Pred. No. 0.052;
7; Mismatches
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COILED COIL (POTENTIAL).
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Bauer C.B., Kuhlman P.A., Bagshaw C.R., Rayment I.;

"X-ray crystal structure and solution fluorescence characterization
of Mg.2'(3')-O-(N-methylanthraniloy1) nucleotides bound to the
Dictyostellum discoideum myosin motor domain.";
J. Mol. Biol. 274:394-407(1997).

-i- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE
ACTIVITY THAT IS ACTIVATED BY ACTIN.
ACTIVITY THAT IS ACTIVATED BY ACTIN.
-i- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES
INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKAI
LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) MEDLINE-98070605; PubMed-9405148;
                                                                                                                                                                                                                                                                                                                                                                                                                           Gulick A.M., Bauer C.B., Thoden J.B., Rayment I.;
"X-ray structures of the MgADP, MgATPgammaS, and MgAMPPNP complexes of the Dictyostellum discoideum myosin motor domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) MEDLINE=97452580; PubMed=9305951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE=96206189; PubMed=8611530;
Smith C.A., Rayment I.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "X-ray structures of the myosin motor discoideum complexed with MgADP.BeFx (Biochemistry 34:8960-8972(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) MEDLINE=95345066; PubMed=7619795;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phosphorylatable heavy chain fragment of Dictyostelium myosin FEBS Lett. 269:239-243(1990).
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                                              <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "X-ray structure of the magnesium(II).ADP.vanadate complex of the Dictyostelium discoideum myosin motor domain to 1.9-A resolution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) MEDLINE-95345067; PubMed-7619796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dictyostelium myosin heavy chain."; FEBS Lett. 227:71-75(1988).
                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry
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Wagle G., Noegel A., Scheel J., Gerisch
"Phosphorylation of threonine residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION SITES.
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[1]
                                        CORTEX.

DOMAIN: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO
  MEROMYOSIN
SPLIT INTO
                                                                                    SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Natl. Acad. Sci.
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  GLOBULAR
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  SUBFRAGMENTS
                                                                                    HIGHEST CONCENTRATION IN
HEAVY MEROMYOSIN SUBFRAGMENTS (S1)
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                                                                                    THE POSTERIOR
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                                                                                                                              (MHC), 2 ALKAL
CHAIN SUBUNITS
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Query Match
Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                            PDB; 1MMD;
PDB; 1MMG;
PDB; 1MMN;
PDB; 1MND;
PDB; 1MNE;
PDB; 1VOM;
PDB; 1LVK;
                                                                     MOD_RES
MOD_RES
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SEQUENCE
                                                                                                                                                                                                                               SMART;
                                                                                                                                             NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are r
                                                                                                                                                                                                Calmodulin-binding;
                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                   ProDom;
                                                                                                                                                                                                                                                                                                    InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR001609; myosin_he
                                                                                                                                     DOMAIN
                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                           Myosin;
                                                                                                                                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                  Pfam;
                                                                                                                                                                                                                                                                                                                                  DictyDb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBFRAGMENT (S2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPT CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: PHOSPHORYLATION INHIBITS THICK FILAMENT FORMATION / THE ACTIN-ACTIVATED ATPASE ACTIVITY.

MISCELLANEOUS: DICTYOSTELIUM MYOSIN II HAS NO K(2)EDTA / ACTIVITY, PERHAPS CORRELATED WITH THE ABSENCE OF A CYS / POSITION (688).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 MYOSIN-LIKE SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                     1MMA;
NKLFFDLAQEEENVLDAE-FLKNELDSVKAQLSQKD---REKRDSQAIIDTLRDTLEERN
                                                                                                                                                                                                                                                                   PF00612; IQ; 2.
PF00063; myosin_head; 1.
PF02736; Myosin_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    м14628;
                                                                                                                                                                                                                             SM00015; IQ; 1.
SM00242; MYSc;
                    l Similarity
67; Conserv
                                                                                                                                                                                                          ; PS50096; IQ; Coiled coil; /
                                                                                                                                                                                                                                                  PR00193; MYOSINHEAVY. PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                   DD01008; mhcA
                                                                                                                                                                                                                                                                                                                                            03-DEC-97.
17-AUG-96.
03-DEC-97.
03-DEC-97.
17-AUG-96.
17-AUG-96.
23-DEC-96.
23-DEC-98.
                                                                      762
817
179
638
738
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130
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1823
1823
2029
2116
                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 S00250
                                                                                                                                                                                                                                                                                                                                                                                                                                         A26655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA33227.1;
                                                                       2029
A; 24
                                                                                           761
791
2116
186
660
752
130
678
1823
                                                                                                                                                                                                Methylation;
                            15.1%;
                                                                                                                                                                                                Actin-binding; ATP-binding; 3D-structure; Methylation; Alkylation; Phosphorylation.
                                                                                                                                                                                                                                                                                                    myosin_head
                                                                       13871
                    52;
                                                                       Œ,
                             Score 162.5;
Pred. No. 0.
                                                                                                                      ACTIN-BINDING.
ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (DI-) (POTENTIAL).
                                                                     PHOSPHORYLATION (BY PHOSPHORYLATION (BY FROSPHORYLATION (BY FROSPHORYLATION)
                                                                                                   ALKYLATION (SH-1)
PHOSPHORYLATION (
                                                                                                                                                                  COILED
                                                                                                                                                                                      MYOSIN
                    Mismatches
                                                                                                                                                                 COIL (POTENTIAL).
                                                                                                                                                                                      HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLOBULAR
                              ; DB
.066;
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MHCK).
CMCK).
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Best Local
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-!-FUNCTION: Involved in DNA double-strand break repair (DSBR). Trad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWI
between
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P58302;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thermoplasma volcanium. Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000875; InterPro; IPR001238; InterPro; IPR003395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified
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                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                       DNA repair; Hydrolase; ATP-binding; NP_BIND 30 37 ATP (B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20570466; PubMed=11121031;
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CT-2001 (Rel. 40, Last sequence update)
CT-2001 (Rel. 40, Last annotation update)
double-strand break repair rad50 ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Forms a complex with mrell (By similarity). SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and/or repositioning DNA ends into the mrell active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                            LKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NVEKSKKTLESQLVAVNNELDEEKKNRD 1111
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MKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLL----QSQRSEVEEMIRDMGVGQSAVE 140
                                                       LKEVIDDLTANVSDYDYLKNELQSKI----NEIDNNNKQIEELESKLRLIEPEIKALEEE
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                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                               895 AA;
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24.3%;
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                                                                                                                                                                                                Score 162; DB 1
Pred. No. 0.029;
                                                                                                                                                                                                                                                                                                            Inding; Coiled coil; Complete ATP (BY SIMILARITY). COILED COIL (POTENTIAL). v; 4A47DA9287E82D3A CRC64;
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P24733;
                              use by non-profit institutions as long as its cont
modified and this statement is not removed. Usage by
entities requires a license agreement (See http://www.
                                                                                                                                                                                                                                      -!- FUNCTION: MUSCLE CONTRACTION.
-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
-!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nyitray L., Goodwin E.B., Szent-Gyorgyi A.G.;
"Nucleotide sequence of full length cDNA for a scallop striated muscle myosin heavy chain.";
Nucleic Acids Res. 18:7158-7158(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nyitray L., Goodwin E.B., Szent-Gyoergyi A.G.;
"Complete primary structure of a scallop striated muscle myosin heavy chain. Sequence comparison with other heavy chains reveals regions that might be critical for regulation.";
J. Biol. Chem. 266:18469-18476(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Structure of the regulatory domain of scaresolution: implications for regulation."; Structure 4:21-32(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Szent-Gyorgyi A.G., Cohen C., Structure of the regulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  x-ray Crystallography (2.8 angstroms) of MEDLINE=94173332; PubMed=8127365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aequipecten irradians (Bay scallop).
Eukaryota; Metazoa; Mollusca; Bivalvia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-1992
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MEDLINE=92011595; PubMed=1917970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin heavy chain, striated muscle.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xie X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91088319; PubMed=2263488;
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                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way fied and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/
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(Rel. 21, Last seq
(Rel. 40, Last ann
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license@isb-sib.ch).

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RESULT 11
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Best Local S
Matches 73
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Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_tail; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
                                                   TANA_XENLA
Q01550;
Q1-JUN-1994
Q1-JUN-1994
16-QCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                            TURN
SEQUENCE
           Tanabin.

Yanabin.

Xenopus laevis (African clawed frog).

Xenopus laevis (African clawed frog).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                         1020
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MOD_RES
MOD_RES
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InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR002017; Spectrin.
InterPro; IPR001609; Myosin_head.
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ATP-binding;
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  Xenopodinae;
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A40997;
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                                                                                                                                                                                                                                                                                                                            KLIMQKADFESQIKELEERLLDEEDAAADLEGIKKKMEADNANLKKDIGDLENTLQKAEQ
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SM00242; MYSC;
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A40997
  Xenopus
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protein; Coiled coil; Thick filament;
protein; Calmodulin-binding; 3D-struc
lkylation; Calmodulin-binding; 3D-struc
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ATP (BY SIMILARITY).

ALKYLATION (SH-1) (BY SIMI ALKYLATION (SH-2) (BY SIMI
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Pred. No. 0.064;
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                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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SIMILARITY)
         Pipidae;
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Matches 57
                                MYSB_CAEEL
P02566;
21-JUL-1986
21-JUL-1986
16-OCT-2001
                                                                                             _CAEEL
         Myosin heavy chain UNC-54 OR MYO-4.
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SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuron 9:417-428(1992).
-!- TISSUE SPECIFICITY: GROWTH CONES OF
-!- DEVELOPMENTAL STAGE: IS EXPRESSED 1
DURING EMBRYOGENESIS IN THE BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hemmati-Brivanlou A., Mann R.W., Harland R.M.; "A protein expressed in the growth cones of emneurons defines a new class of intermediate fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Tadpole head;
MEDLINE=92398961; PubMed*1524825;
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. The The Theorem 1975 institutions as long
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58; Mismatches
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N, CRANIAL NERVES, AND SPINAL
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filament protein.";
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MCLachian A.D., karn J.;
"Periodic charge distributions in the
"Periodic charge spacings in muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=83273600; PubMed=6576334;
Karn J., Brenner S., Barnett L.;
"Protein structural domains in the Caenorhabditis elegans unc-54
myosin heavy chain gene are not separated by introns.";
Proc. Natl. Acad. Sci. U.S.A. 80:4253-4257(1983).
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J01050; AAA28124.1;
EMBL; V01494; CAA24738.1;
PIR; A02992; MWKW.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           match cross-bridge spacings in Nature 299:226-231(1982).
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Rhabditidae;
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DOMAIN
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                                                                                                                                               SMART; SM00242; MYSc;
Myosin; Muscle protei
                                                                                                                                                                                          PRINTS; PR00193; MYOSINHEAVY PRODOM; PD000355; myosin_heav
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InterPro; IPR002928; Myosin_tail
InterPro; IPR001609; Myosin_head
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                                                                                                                      ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                          HSSP;
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MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS C.ELEGANS.

C.ELEGANS.

MISCELLANEOUS: MHC A AND MHC B ARE FOUND EXCLUSIVELY IN THE WALL MUSCLE. THEY CO-ASSEMBLE INTO BODY WALL THICK FILAMENT.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOWAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
PYM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: MÜSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS
HEAVY CHAIN SUBUNITS (MIC), 2 ALKALI LIGHT CHAIN SUBUNITS (MAC-2).
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes sup-7 X and sup-5
                                                                                                                                                                                                                                     PF00063; myosin_head; 1.
PF02736; Myosin_N; 1.
PF01576; Myosin_tail; 1.
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and this statement
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                                                                                                                         Methylation;
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PubMed=7202124;
                                                                                                                                                                                          myosin_head; 1.
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                         ALPHA-HELICAL HINGE.
                                             MYOSIN HEAD-LIKE.
COILED COIL (POTENTIAL)
ALPHA-HELICAL TAILPIECE
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Myosin heavy chain, smooth muscle isoform (
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MOD_RES
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SEQUENCE
                                TISSUE-Uterus;
MEDLINE-96172919; PubMed-8593698;
Suzuki T., Kim H.S., Kurabayashi M., Hamada H., Fujii H., Aikawa M.,
Watanabe M., Watanabe N., Sakomura Y., Yazaki Y., Nagai R.;
Watanabe M., Watanabe N., Sakomura Y., Yazaki Y., Nagai R.;
"Preferential differentiation of P19 mouse embryonal carcinoma cells
into smooth muscle cells. Use of retinoic acid and antisense against
into smooth muscle cells. Use of retinoic acid and antisense against
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DOMAIN
DOMAIN
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Miano J.M., Cserjesi P., Ligon K.L., Periasamy M., C
"Smooth muscle myosin heavy chain exclusively marks
lineage during mouse embryogenesis.";
Circ. Res. 75:803-812(1994).
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the central nervous system-specific
Circ. Res. 78:395.404(1996).
-!- FUNCTION: MUSCLE CONTRACTION.
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Hasegawa K., Arakawa E., Oda S.,
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE=Uterus;
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Mammalia; Eutheria;
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Rodentia;
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ALKYLATION (SH-2).
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I -> L (IN REF. 2).
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                              Matsuda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               isoform (SN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                              murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .079;
                                                                                                                                                                                                                                                                                                                                              Υ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
   PROTEIN THAT CONSISTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMMHC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                              smooth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -TLDDLEDSLEREKRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                          Olson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1966
                                                                                                                                                                                                                                                                                                                              muscle myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
Murinae; Mus
                                                                                                                                                                                                            smooth
                                                                                                                                                                                                                        Ħ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
   OF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9;
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밁
                   Q
                                                                                             Matches
                                                                                                                                                                                                                                                                                                                      Pfam; PF00612; IQ; 1.
Pfam; PF0063; myosin_head; 1.
Pfam; PF02736; myosin_N; 1.
Pfam; PF01576; myosin_tail; 1.
Pfam; PF01576; myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1
 1688
                                                                                           CONFLICT
SEQUENCE
                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin; Muscle protein; Coiled coil; T
Calmodulin-binding; ATP-binding; Methy
Multigene family; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                    MGD;
                                                                                                                                                VARSPLIC
                                                                                                                                                                               MOD_RES
                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                             NP_BIND
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                             PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                  SMART;
                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
InterPro; IPR002928; Myosin_tail.
InterPro; IPR001609; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
                    10 DLAQEEENVLDAEFLKNELDSVKAQLSQK-----
                                                                                                                                                           RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
DLMQLQEDLAAAERARKQADLEKEELAEELASSLSGRNTLQDEKRRLEARIAQLEEELEE 1747
                                                                                                                                                                                                                                                                                                                                                                                                                                                      D85923;
D85924;
L25860;
S81516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                              P10587;
                                                                                                                                                                                                                                                                                                        SM00015; IQ; 1
SM00242; MYSC;
                                                   Similarity
                                                                                                                                               786
844
1935
178
661
762
129
701
711
1930
                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAA19691.1; -. AAA67552.1; -. AAB36168.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                               1BR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAA19690.1; -.
                                                                                             ŞĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                    Myh11
                                                                                                                                                785
815
1934
1972
185
683
776
129
701
711
                                                                                                                 126
161
                                                  14.9%;
                                                                                             227026
                                                                                         METHYLATION (TRI-) (POTENTIAL).

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

RGNEASFVPSRRAGGRRVIENTDGSEEMDARDSDFNGTKA
SE -> GPPPQETSQ (IN ISOFORM 2).

N -> D (IN REF. 3).
A -> V (IN REF. 2).
Q -> K (IN REF. 2).

Q -> K (IN REF. 2).
                                       Score 160; DB
Pred. No. 0.08
53; Mismatches
                                                                                                                                                                                                                               IQ. COILED COIL (POTENTIAL).
                                                                                                                                                                                       ACTIN-BINDING ACTIN-BINDING
                                                                                                                                                                                                           ATP (POTENTIAL)
                                                                                                                                                                                                                      CARBOXYL-TERMINAL.
                                                                                                                                                                                                                                                    MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                      oil; Thick filament; Actin-binding; Methylation; Alkylation;
                   -----DREKRDSQAIIDTLRDTLEE
                                                  DB 1.084;
                                                                                                                                                                                      (BY SIMILARITY). (BY SIMILARITY).
                                                           1;
                                                            Length 1972;
                                        Indels
                                        48;
                    58
                                        7;
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RESULT 14
KINH_HHAM
ID HAM KINH_H AC
P33176
DT 01-OCT
DT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94242....

MICLAS J., Navone F., Hom-bounce.

"Cloning and localization of a conventional Alice."

"Cloning and localization of a conventional Record of the Conventional Record of the Conventions of the Conventions of the Convention of the Conventional Record of the Convention of the Convent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1993 (Rel. 27,
01-OCT-1993 (Rel. 27,
16-OCT-2001 (Rel. 40,
Kinesin heavy chain (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KINH_HUMAN P33176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE SPECIFICITY.
MEDLINE=94242426; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kull F.J., Sablin E.P., Lau R., Fletterick R.J., Vale R.D.; "Crystal structure of the kinesin motor domain reveals a strininal to myosin."; Nature 380:550-555(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF MEDLINE=96195066; PubMed=8606779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interaction of the COOH-terminal domain with cytoplasmic microtubules in transfected CV-1 cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Navone F., Niclas J., Ho
McCaffrey G., Vale R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-92299683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KIF5B OR KNS1 OR KNS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell Biol. 117:1263-1275(1992).
                                                                                                                                                                                                                                    AND THE PROCESSES IN THE NEURONS.

TISSUE SPECIFICITY: FOUND IN NEWBORN AND ADULT BRAIN, LIVER, KIDNEY, SPLEEN, HEART, LUNG AND SCIATIC NERVE.

RIDNEY, SPLEEN, HEART, LUNG AND SCIATIC NERVE.

DOMAIN: COMPOSED OF THREE STRUCTURAL DOMAINS: A LARGE GLOBULAR TERMINAL DOMAIN WHICH IS RESPONSIBLE FOR THE MOTOR ACTIVITY OF KINESIN (IT HYDROLYZES ATP AND BIBLE FOR THE HEAVY CHAIN ALPHA-HELICAL COILED COIL DOMAIN THAT MEDIATES THE HEAVY CHAIN DIMERIZATION; AND A SMALL GLOBULAR C-TERMINAL DOMAIN WHICH
                                                                                        SUBFAMILY.
                                                                                                                                                                INTERACTS WITH OTHER PROTEINS (SUCH AS VESICLES AND MEMBRANOUS ORGANELLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNALKSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VKAKLKSTVAALEAKIAQLEEQVEQEAREK - - - QAATKSLKQKDKKLKEVLLQVEDERK -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LKCKMK-TMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITSLRKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQGNMEAMSDRVRKATLQAEQLSNELATERSTAQKNESARQQLERQNKELRSKLQEVEGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MAEQYKEQAEKGNTKVKQLKRQLEEAEEESQCINANRRKLQRELDEATESNEAMGRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and expression of a human kinesin heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1607388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7, Last sequence update)
0, Last annotation update)
_(Ubiquitous kinesin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hom-Booher N.,
                                                                                                                            ТО
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -Booher N., Vale R.D.;
of a conventional kinesin motor expressed
                                                                                                                            THE
                                                                                                                            KINESIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                motor domain reveals a structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sparks L., Bernstein H.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               963
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                                                                                                                                                                                                        THE
                                                                                                                            PROTEIN FAMILY.
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Best Local
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NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1.
PROSITE; PS50067; KIRESIN_MOTOR_DOMAIN2; 1.
MOTOR protein; Microtubules; Arbinding; Coiled DOMAIN 1 256 KINESIN-MOTOR.
DOMAIN 329 914 COILED COIL.
DOMAIN 315 963 GLOBULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                           MEDLINE-99425770; PubMed-10493829;
Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell Eichler E.E., Harris P.C., Venter J.C., Adams M.D.; "Genome duplications and other features in 12 Mb of DNA shuman chromosome 16p and 16g.";
                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-1994 (Rel. 29, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Myosin heavy chain, smooth muscle isoform (
MYH11 OR KIAA0866.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001752; kinesin. Pfam; PF00225; kinesin; 1. PRINTS; PR00380; KINESINHEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A41919;
PDB; 1BG2; 1
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  MEDLINE=99156230;
                           SEQUENCE OF 1-1266
TISSUE-Brain;
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE-99425270;
                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00129; KISc;
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57; Conser
                                                                                                        60:295-308(1999).
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  PubMed=10048485;
                                                       FROM N.A.
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muscle isoform (SM
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Pred. No. 0.046;
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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A1FE5760C3250C8B
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                                                                                                                                                          of DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coil; 3D-structure
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                                                                                                                                                                                                           S.,
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AND 2 REGULATORY LIGHT CHAIN SUBURITS (MLC.2)

AND 2 REGULATORY LIGHT CHAIN SUBURITS (MLC.2).

-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-!- TISSUE SPECIFICITY: SMOOTH MUSCLE; EXPRESSED IN THE UMBILICAL ARTERY, BLADDER, ESOPHAGUS AND TRACHEA.

-!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

-!- PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-!- DISEASE: A CHROMOSOMAL REARRANGEMENT, KNOWN AS PERICENTRIC INVERSION INV(16) [P13022], PRODUCES A FUSION PROTEIN THAT CONSISTS OF THE 165 N-TERMINAL RESIDUES OF CBF-BETA (PEPB2) WITH THE TAIL REGION OF MYHLI. THIS REARRANGEMENT IS ASSOCIATED WITH ACUTE MYELOID LEUKEMIA OF MAED SUBSTYPE.
-!- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRACMENT (S2).
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
                                                                                                                                          PRINTS;
ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00063; myosin_head; 1. pfam; PF01576; Myosin_tail; 1. PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. The complete sequences of 100 new cDNA clones from brain which coffor large proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>:</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Hippocampus;
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"Human smooth muscle myosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF
                    Myosin; Muscle protein; Coiled co
                                                                                                                                                                                                                                            Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                       InterPro; IPR002928;
InterPro; IPR002017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The Theorem Theorem 19 The Theorem 1997 to the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1093-1972
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                                                                     PROSITE;
                                                                                                                                                                                                                                                                   InterPro; IPR001609;
                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                 HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                         L; AF001548; AAC31665.1; -.
L; U91323; AAC35212.1; -.
L; AB020673; BAA74889.1; -.
L; D10667; -; NOT_ANNOTATED_CDS.
L; X69292; CAA49154.1; -.
P; P08799; IMMN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                       160745;
                                                                     ; PD000355; myosin_head; sm00015; IQ; 2. sm00242; MYSC; 1. E; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           smooth muscle 16q12.";
family; Proto-oncogene;
                                                                                                                                                                                                                                                                                                                                             IPR000048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genet. 46:61-67(1993).
                                                                                                                                                                                                                                                                   myosin_head
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                                                                                                                                                                                                                                                                                               Spectrin
                                                                                                                                                                                                                                                                                                                    Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FROM
                                              Coiled coil; Thick filament; Actin-binding;
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                       Methylation;
  Chromosomal
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P35748;
01-JUN-1994
01-FEB-1996
16-OCT-2001
                                                                                                         gene:
                                                                                                                                                                                    MYHII.
Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
"```mmalia` Rutheria; Lagomorpha; Leporidae; Oryctolagus.
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Babij P., Kelly C., Periasamy M.;
"Characterization of a mammalian smooth muscle myosin heavy-chain
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e: complete nucleotide and protein coding sequence and analysis of 5' end of the gene.";
5' end of the gene.";
c. Natl. Acad. Sci. U.S. A. 88:10676-10680(1991).
FUNCTION: MUSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).
SUBCELULAR LOCATION: Thick filaments of the myofibrils.
SUBCELULAR LOCATION: Thick filaments of the myofibrils.
DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
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ALKYLATION (SH-2) (POTENTIAL).
EEK -> NSE (IN REF. 3).
ELQS -> TLSF (IN REF. 2).
T -> S (IN REF. 3).
KQ -> NE (IN REF. 3).
A -> S (IN REF. 4).
T -> L (IN REF. 3).
MW; 67665BB2AECE1277 CRC64;
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Pred. No. 0.09
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ACTIN-BINDING (BY SIMILARITY).
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smART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
pROSITE; pS50096; IQ; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Myosin; Muscle protein; Coiled coil; Thick filament; Acti
Calmodulin binding; ATP-binding; Methylation; Alkylation
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InterPro; IPR001609;
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MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
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ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (FOR SIMILARITY).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
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Pred. No. 0.095;
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COILED COIL (POTENTIAL).
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1921 VNALKSK 1927

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _ARCFU STANDARD; PRT;
RA50_ARCFU STANDARD; PRT;
029230;
16-OCT-2001 (Rel. 40, Last sequence u
16-OCT-2001 (Rel. 40, Last annotation
DNA_double-strand break repair rad50
                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                          InterPro; IPR001238; RecF.
InterPro; IPR002017; Spectrin.
Pfam; PF00470; RecF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
Nature 390:364-370(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=VC-16 / DSM 4304 / ATCC 49558; MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAD50 OR AF1032.
Archaeoglobus fulgidus
                                                                                                                                                                                                                                     DNA repair; Hydrolase; ATP-binding; Coiled coil; Complete proteome.

NP_BIND
38 AFF (BY SIMILARITY).

DOMAIN
148 728 COILED COIL (POTENTIAL).

SEQUENCE 886 AA; 103633 MW; D35641D499AA8B58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaeoglobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR003439;
 267
                                                                        207
                                    50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    similarity).
SUBUNIT: Forms a complex with mrell (By similarity).
SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Involved in DNA double-strand break repair (DSBR). The rad50/mrell complex possesses single-strand endonuclease activity and ATP-dependent double-strand-specific exonuclease activity. Rad50 provides an ATP-dependent control of mrell by unwinding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and/or repositioning DNA ends into the mrell active
ERIED-LEKKAKEVKELKPKAERYSILEKLLSEINQALRDVEKREGDLTREAAGIQAQLK
                                    DTLRDTLEERNATVESLQNALNK---AEMLCSTLKKQMKFLEQR------
                                                                      ESLREKLSEEVRNLESRLKELEEHKSRLESLRKQESSVLQEVRGLEEKLRELEKQLKEVV
                                                                                                         KTIINKLFFDLAQEEENVLDAEFLKNELDSVKAQ-----
                                                                                                                                                                                                                                                                                                                                                                                       AF1032;
                                                                                                                                                                                                                                                                                                                                                                                                        AE001032; AAB90211.1; -.
                                                                                                                                                                Similarity
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40, Last sequence update 40, Last annotation update
                                                                                                                                                                                                                                                                                                                                                    ABC_transportr
Recf.
                                                                                                                                                                14.78;
22.38;
                                                                                                                                             Score 157.5;
Pred. No. 0.05
71; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n update)
ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                886
                                                                                                                                                             .051;
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                                                                                                         -----LSQKDRE-KRDSQAII
                                                                                                                                                                              Length
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                                                                                                                                                                                  886;
                                                                                                                                             41;
                                    -QDETK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou L.,
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                                                                                                                                             Gaps
                                    95
                                                                      266
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RESULT 18
MYSN_ACACA
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                                                                      Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00736; Myosin_N; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM000442; MYSG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete nucleotide sequence and deduced polypeptide sequence of a nonmuscle myosin heavy chain gene from Acanthamoeba: evidence of a hinge in the rodlike tail.";
J. Cell Biol. 105:913-925(1987).
-!- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO F-ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY F-ACTIN.
-!- SUBUNIT: MYOSIN II HEAVY CHAIN IS TWO-HEADED. IT SELF-ASSEMBLES INTO FILAMENTS. HEXAMER OF 2 HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2 REGULATORY LIGHT CHAIN SUBUNITS
                                                                                                                                                                                                                                                                                                                                                EMBL; Y00624; CAA68663.1;
PIR; A27224; A27224.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MLC-2).

(MLC-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P05659;
01-NOV-1988
PROSITE; PS50096; IQ; Myosin; Coiled coil; Amposin; Alkylation; Alkylation
                                                                                                                                                                                                                                                                                           InterPro; IPR000048;
InterPro; IPR004009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE=87308395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Acanthamoebidae; Acanthamoeba. NCBI_TaxID=5755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myosin II heavy chain, non muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYSN_ACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Acanthamoeba castellanii (Amoeba)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1988
                                                                                                                                                                                                                                                                       InterPro; IPR001609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           III, Bowers B.,
2d coil; Actin-binding; ATP-binding; Calmodulin-binding;
Alkylation; Phosphorylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
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40, Last annotation
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                                                                                                                                                                                                                                                                                              IQ.
Myosin_N
                                                                                                                                                                                                                                                                  myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paterson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     son B.M., Korn E.D.; deduced polypeptide from Acanthamoeba:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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Best Local
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Sohda M., Misumi Y., Yano A., Takami N., Ikehara Y.;

"Phosphorylation of the vesicle docking protein pll5 regulates its
association with the Golgi membrane.";

J. Biol. Chem. 273:5385-5388(1998).

-i- FUNCTION: GENERAL VESICULAR TRANSPORT FACTOR REQUIRED FOR
INTERCISTERNAL TRANSPORT IN THE GOLGI STACK; IT IS REQUIRED FOR
TRANSCYTOTIC FUSION AND/OR SUBSEQUENT BINDING OF THE VESICLES TO
THE TARGET MEMBRANE. MAY WELL ACT AS A VESICULAR ANCHOR BY
INTERACTING WITH THE TARGET MEMBRANE AND HOLDING THE VESICULAR
AND TARGET MEMBRANES IN PROXIMITY (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: PERIPHERAL MEMBRANE PROTEIN WHICH RECYCLES
BETWEEN THE CYTOSOL AND THE GOLGI APPARATUS DURING INTERPHASE.
                                                                                                                                                                                                                                                                                                  VDP_HUMAN
060763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOD_RES
MOD_RES
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP_BIND
DOMAIN
DOMAIN
                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
General vesicular transport factor pll5 (Transcytosis protein) (TAP) (Vesicle docking protein).
                                                                                                                                                                                                                                                                                                                                                                                                                      1197
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DOMAIN
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DOMAIN
                                                                                                                                              MEDLINE-98148093;
                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                        1257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AR----EEAHRLKCKMKTMEQIELLLQSQ-----RSEVEEMIRDMGVGQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKDREKRDSQAIIDTLRDTLEERNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLAQEEENVLD------AEFLKNELDSV-----
                                                                                                                                                                                                                                                                                                                                                                       LEGELERLEEELLTAQEARAAEKNLDKANLELEELRQEADD
                                                                                                                                                                                                                                                                                                                                                                                           LNTELDQAKLELRSAQ-----KDLQSADQEITSLRKKSDD
                                                                                                                                                                                                                                                                                                                                                                                                                   LEKERKNALDEVAQLTADLDAERDSGAQQRRKLNTRISELQSELENAPKTGGASSEEVKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VRANVDKQKKALEAKLTELEDQVTALDGQKNAAAAQAKTLKTQVDETKRRLEEAEASAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEKSGKEAASSKAKQLGQQLEDARSEVDSLKSKLSAAEKSLKTAKDQNRDLDEQLEDERT 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          -SAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLV-----SSRSKLKT
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790
848
848
1227
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1483
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1660
7660
7660
7640
133
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1494
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                                                                                                                                             PubMed=9478999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 156.5;
Pred. No. 0.09
9; Mismatches
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ALKYLATION (SH-1)
PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION. W; 2CE49BE51173D17E
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ALPHA-HELICAL TAILPIECE
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                                                                                                                                                                                         Craniata; Vertebrata; Catarrhini; Hominidae.
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Matches 64
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01-JUN-1994
16-OCT-2001
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                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                            MYSA_DROME P05661;
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           Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between
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PTM: PHOSPHORYLATED IN A CELL CYCLE-SPECIFIC MANNER;
PHOSPHORYLATED IN INTERPHASE BUT NOT IN MITOTIC CELLS.
DEPHOSPHORYLATED PROTEIN ASSOCIATES WITH THE GOLGI MEMBRANE;
PHOSPHORYLATED PROMOSTES DISSOCIATES.
PHOSPHORYLATION PROMOSTES DISSOCIATION.
SIMILARITY: BELONGS TO THE VDP/USO1/YBL047C FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European
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                                                                                                                                                                                                      QDDLLVLLADQDQKILSLKNKLKD
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sen the Swiss Institute of Bioinformatics and the EX
European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                         QVAELKQELATLKSQLNSQSVEITKLQTEKQELLQKTEAFAKSVEVQGETETIIATKTTD
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Pred. No. 0.
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; 2E748F2C1BC2B942 CRC64;
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[1]
SEQUENCE FROM N.A.
MEDLINE=89384556; PubMed=2506434;
MEDLINE=8938456; PubMed=2506434;
Decrease E.L., Ober M.B., Emerson C
                                                                                                                                                                                                                                                                                                                                                                                     the Euro
                                                                                                                                    FlyBase; FBgn0002741; Mhc.
InterPro; IPR000048; IQ.
InterPro; IPR004009; Myosin_N.
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                                                                                                                                                                              HSSP;
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                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CANTON-S: TISSUE=Embryonic muscle; MEDLINE=91330870; PubMed=1907912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 George E.L., Ober M.B., Emerson C.P. Jr.; Functional domains of the Drosophila melanogaster muscle myosin heavy-chain gene are encoded by alternatively spliced exons."; Mol. Cell. Biol. 9:2957-2974(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                This
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                                 ProDom; PD000355; myosin_head;
                                                                                                                InterPro;
                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kronert W.A., Edwards K.A., Roche E.S., Wells L., Bernstein S.I., "Muscle-specific accumulation of Drosophila myosin heavy chains:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  intron
                                                                                                                                                                        IL; M61229; AAA28686.1; A

IL; M61229; AAA28687.1; A

IL; J02788; AAA28707.1; A

IL; J02788; AAA28707.1; A

IL; X60196; CAA42752.1; A

IL; X60196; CAA42753.1; A

IL; X60196; CAA42754.1; A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBURIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSIST
HEAVY CHAIN SUBURITS (MHC), 2 ALKALI LIGHT CHAIN SUBURITS
AND 2 REGULATORY LIGHT CHAIN SUBURITS (MLC-2).

SUBECLICIAR LOCATION: Thick filaments of the myofibrils.
ALTERNATIVE PRODUCTS: AS DROSOPHILA HAS A SINGLE MUSCLE MMCC ISOFORMS MUST RELY ON ALTERNATIVE RNA SPLICING THAT LE
DIFFERENCES IN THE C-TERMINUS OF THE VARTOUS MHC PROTEINS.
MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1
MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATE
SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBFRAGMENT (S2).
SIMILARITY: CONTAINS
SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                                                                                                                                                   ween the Swiss Institute of Bioinf
European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright.
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                                                                                   PF00063; myosin_head; 7.
            SM00015;
SM00242;
                                                                                                                                                                                                                                                                                                                                   s requires a license agreement (S
an email to license@isb-sib.ch).
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IPR004009;
IPR002928;
IPR001609;
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         IQ; 1
MYSc;
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                                                                                                             myosin_head
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_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
VARSPLIC
VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2113
"A novel gene, AF-1p, fused to HRX in t(1:11)(p32 related to AF-4, AF-9 nor ENL."; Oncogene 9:1039-1045(1944).

-i- FUNCTION: INVOLVED IN CELL GROWTH REGULATION. SIGNAL TRANSDUCTION AND MITOGENICITY. SIGNAL TRANSDUCTION AND MITOGENICITY.
-i- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-i- TISSUE SPECIFICITY: UBIQUITOUSLY EXPRESSED.
                                                                                      SEQUENCE FROM N.A.
MEDLINE-94181254; PubMed-8134107;
Bernard O.A., Mauchauffe M., Mecu
                                                                                                                                      "The human eps15 gene, encoding conserved in evolution and maps Oncogene 9:1591-1597(1994).
                                                                                                                                                                                                                                                                                                                          01-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2233
                                                                                                                                                                      Wong W.T., Kraus M.H., Carlomagno F., Croce C.M., Huebner K., di Fiore P.P.;
                                                                                                                                                                                         TISSUE=Melanoma;
MEDLINE=94239734; PubMed=8183552;
                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                            Epidermal growth
                                                                                                                                                                                                                                                                                                                                                01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                          P42566;
                                                                                                                                                                                                                                                                                                                                                                       EP15_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                            2353 EAEERADLAEQAISKFRAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myosin; Muscle
ATP-binding; Ca
                                                                               Berger
                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                       EPS15 OR AF1P.
                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                    S-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALEQQIKELQVRLDEAEANALKGGKKAIQKLEQRVRELENELDGEQRRHADAQKNLRKSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDAREQLGISERRANALQNELEESRTLLEQADRGRRQAEQELADAHEQLNEVSAQNASIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RRVKELSFQSEEDRKNHERMQDLVDKLQQKIKTYKRQIEEAEEIAALNLAKFRKAQQELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KATGELA-----DRLK-----KDLVSS-RSKLKTLNTELDQAK-----LELRSAQKDLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVEEMIRDMGV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NALNKAEMLCSTLKKQMKFL----EQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLAQEEENVLD--AEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAKRKLESELQTLHSDLDELLNEAKNSEEKAKKAMVDAARLADELRAEQDHAQTQEKLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 22.8
59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1205
1233
227
2385
2386
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                                                                                                                                                                                                                                                                                                            (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
rowth factor receptor substrate 15
                                                                                                                                                                                                                                                                           (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQEITSLRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Calmodulin-binding; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1232
2376
234
2385
2411
                                                                                                                                                                                                                                                   Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 154.5; DE Pred. No. 0.21; 56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GQSAVEQLAVYCVSLKKEYE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILARITY).
P -> I (IN SHORT ISOFORM).
MISSING (IN SHORT ISOFORM)
EK -> RE (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IQ.
                                                                                           Mecucci
                                                                                                                                                                                                                                                     Craniata; Vo
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                  a tyrosine kinase substrate, to 1p31-p32.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8C4FEC1BB8D310A9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COIL (POTENTIAL).
SIMILARITY).
                                                                                         С.,
                                                                                                                                                                                                                                                                                                                                                                       896
                                                                   t(1;11)(p32;q23),
                                                                                                                                                                                  Zelano A.,
                                                                                                                                                                                                                                                               Vertebrata;
                                                                                           van
                                                                                                                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
                                                                                                                                                                                                                                                                                                              15
                                                                                           den
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Protein
                                                                                          Berghe
                                                                                                                                                                                   Druck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                Euteleostomi;
                                   PLAY A
                                                                                                                                                                                                                                                                                                              EPS15) (AF-1P
                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2411;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                     not
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Best Local S
Matches 53
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SEQUENCE
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between
the Euro
                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
HSSP;
                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
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REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                 REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                           CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                     CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                            Proto-oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00036; efhand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002048; EF-h
InterPro; IPR00261; EPS1
InterPro; IPR003903; UIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities
441
                  182
                                                                                                            312
                                                                                          65
                                                                                                                               10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content if ified and this statement is not removed. Usage by ancities requires a license agreement (See http://www.isb-sities.requires a license agreement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ROGUE ACTIVATOR PROTEIN.
SIMILARITY: CONTAINS 1 EH DOMAIN.
SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: PHOSPHORYLATED ON TYROSINE BY EGFR.
DISEASE: INVOLVED IN A T(1;11)(P32,Q23) CHROMOSOMAL TRANSLOCATION IN ACUTE LEUKEMIAS CAUSING FUSION TO THE TRITHORAX (MLL OR HRX) GENE PRODUCT WHICH CONTAINS DNA-BINDING MOTIFS RESULTING IN A ROGUE ACTIVATOR PROTEIN.
                                                                                                                          DLAQEEENVLD----AEFLK-NELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              600051
STYEEELAKAREELSRLQQETAELEESVESGKAQLEPLQQHLQDSQQEISSMQMK
                   KTLNTELDQA-----
                                    VQELLDELDEQKAQLE
                                            SLQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHRLKCKMKTMEQIELLLQSQRSE
                                                                                                           DRASLQKNIIGSSPVADFSAIKELDTLNNEIVDLQREKNNVEQDLKEKEDTIKQRTSEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U07707; AAA52101.1;
Z29064; CAA82305.1;
P02633; IBOD.
                                                                                                                                                 Similarity
53; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                      SM00054; EFh; 3
SM00027; EH; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                               PS00018;
                                                                                                                                                                                              822
896
                                                                                                                                                Conservative
                                                                                                                                                                                                                          173
236
599
5599
6623
6634
6640
6640
6651
6651
7099
8044
7132
                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                     Calcium-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                              EF_HAND;
                                                                                                                                                                                              822
98673
                                                                                                                                                                                                                         14.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EF-hand.
EPS15_repeat.
                                                                                                                                                                                              MW;
                                                                                                                                                42;
                                                                                                                                               Score 154; DB:
Pred. No. 0.08;
42; Mismatches
                                                                                                                                                                                                     PHOSPHORYLATION (POTENTIAL).
M -> I (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                 EF-HAND 1
EF-HAND 2
15 X 3 AA
                                                                        -QRENTNLQK---
                                                                                                                                                                                                                                            1.
3.
3.
5.
5.
6.
7.
7.
110.
110.
113.
113.
                                                                                                                                                                                                                                  PRO-RICH
                                                                                                                                                                                              -> I (IN REF. 2)
Alb9FB04A07FABEB
                ---KLELRSAQKDLQSADQEITSLRKK
                                   EQLKEVRKKCAEEAQLISSLKAELTSQESQI
                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
REPEATS OF D-P-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                      Chromosomal translocation;
                                                                                                                                                                  ۳.
                                                                                                                                                                                                                         (BY
                                                                                                                                                60;
                                                                                                                                                                 Length 896
                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                        TYR-KINASES)
                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL outstation
                                                                        LQAQKQQ
                                                                                                                                                80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                              Gaps
                                   440
                                                                                        124
                                                                                                           371
                                                                                                                             64
                                                                        393
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RESULT 22

MYHA_HUMA_HIMA MYHA_HIMA MYHA_HUMA MYHA_HUMA MYHAA_HIMA MYHAA_HIMA MYHAA_HIMA MYHAA_HIMA MYHAA_HIMA MYHAA_HIMA MYHAA MAA MAA MAA MAA MAA MA
                                                                                                                                                                                                                                                                                                                 InterPro; IPR004009; InterPro; IPR002928; InterPro; IPR002017; InterPro; IPR001609; InterPro; IPR001609;
  Myosin;
Coiled c
DOMAIN
DOMAIN
                                                                                                                                                                       PRINTS;
ProDom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           on different chromosomes.";
Circ. Res. 69:530-539(1991).
-1- FUNCTION: CELLULAR MYOSIN APPEARS TO I
CELL SHAPE, AND SPECIALIZED FUNCTIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phillips C.L., Yamakawa K., Adelstein R.S.; "Cloning of the cDNA encoding human nonmuscle myosin heavy analysis of human tissues with isoform-specific antibodies. J. Muscle Res. Cell Motil. 16:379-389(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYHA_HUMAN
P35580;
                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; B61231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simons M., Wang M., McBride
Gdula D., Adelstein R.S., We
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 63-722 FROM N.A MEDLINE=91316803; PubMed=18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P08799;
MIM; 160776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-96025307; PubMed-7499478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B). MYH10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAPPING.

SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC-2).

REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE. CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEP CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEP CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                          PF00612; IQ; 1.
PF00063; myosin_head; 1.
PF012736; Myosin_N; 1.
PF01576; Myosin_tail; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M69181; AAA99177.1;
; ATP-binding; Calmodulin-binding; Actin-binding; coil; Alkylation; Multigene family.

1 785 NOSIN HEAD-LIKE.
786 815 IQ.
                                                                                                                   ; PR00193; MYOSINHEAVY.
; PD000355; myosin_head;
SM00015; IQ; 1.
SM00242; MYSC; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D., Adelstein R.S., Weir L.; nonmuscle myosin heavy chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heavy chain,
                                                                                               PS50096; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pean Bioinformatics Institute. The non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 29, Created)
(Rel. 33, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            в61231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1LVK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=1860190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0, Last annotation update)
nonmuscle type B (Cellular myosin
                                                                                                                                                                                                                                                                                                                                        Myosin_N.
Myosin_tail.
Spectrin.
                                                                                                                                                                                                                                                                                                               myosin_head
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SEQUENCE
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21-JUL-1989 (Rel. 12, Last sequence up
16-OCT-1989 (Rel. 40, Last annotation
Myosin heavy_chain D (MHC D).
                                                 SEQUENCE OF 115-365 AND 1492-1763 MEDLINE-85201409; PubMed=3888374; Marn J., Dibb N.J., Miller D.M.; "Cloning nematode myosin genes."; Cell Muscle Motil. 6:185-237(1985)
                                                                                                                                                       myosin
Proc. N
                                                                                                                                                                                                                                                                                         Dibb N.J., Maruyama I.N., Krause M., Karn J.;
"Sequence analysis of the complete Caenorhabditis elegans
heavy chain gene family.";
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-89178677; PubMed-2926820;
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   SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
                                                                                                                                                                                       "Protein
                                                                                                                                                                                                         Karn J., Brenner S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6239;
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64; Conservative
                                                                                                                                                                     structural domains in the Caenorhabditis elegans eavy chain gene are not separated by introns.";
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Acad. S
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Sci. U.S.A. 80:4253-4257(1983).
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ATP (POTENTIAL).
ALKYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
MW; B2BB87FF35EA124F CRC64;
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 SELECTION OF THE PROPERTY OF T
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSIN_HEAVY.
Pr0Dom; PD000355; myosin_head; 1
SMART; SM00242; MYSC; 1.
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Submitted (APR-1996)
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InterPro; IPR002928; Myosin_tail
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 SEQUENCE
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            METHYLATION (TRI-).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
F -> E (IN REF 2).
F -> E (IN REF 2).
V -> D (IN REF 4).
DV -> GD (IN REF 4).
V -> N (IN REF 2).
V -> G (IN REF 2).
V -> G (IN REF 2).
V -> G (IN REF 2).
C -> G (IN REF 2).
C -> G (IN REF 2).
C -> G (IN REF 3).
C -> O (IN REF 3).
C -> O (IN REF 3).
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ALPHA-HELICAL TAILPIECE (SHORT S2) LIGHT MEROMYOSIN (LMM). COILED COIL (POTENTIAL).

RODLIKE TAIL (S2 AND LMM DOMAINS)

MYOSIN HEAD-LIKE

ATP (BY SIMILARITY). ACTIN-BINDING.

CRC64;

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-I- SUBUNIT: MUSCLE MYOSIN IS À HEXAMERIC PROTEIN THAT CONSISTS OF 2
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
AND 2 REGULAPORY LIGHT CHAIN SUBUNITS (MLC-2).

-I- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
-I- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE PHARYNGEAL MUSCLE.
-I- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
-I- PUN: TWO CYSTERINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY
ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
-I- MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT
MEROMYOSIN (LAMY) AND 1 HEAVY MEROMYOSIN (HAM). IT CAN LATER RE
entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                            the European Biointormatics Institute.
                                                                                                                                                                                                                                                                     MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CH. C. ELEGANS.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                           MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CASPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND SUBFRAGMENT (S2).
                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                          FOUR DIFFERENT MYOSIN HEAVY CHAINS
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-I- FUNCTION: THIS PROTEIN BINDS THE HIV-1 TATA ELEMENT AND INHIBI TRANSCRIPTIONAL ACTIVATION BY THE TATA-BINDING PROTEIN (TBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _HUMAN
                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000
30-MAY-2000
16-OCT-2001
                                                                                                                                                       Transcription regulation;
DOMAIN 439 922
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                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    923
            11 LAQEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQATIDTLRDTL---EERNATVESLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QNKQLEIQQDNNKKKDSEIIKFRRDLDE 1187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EENVLDAEFLKNELDSVKAQLSQKDRE------KRDSQAIIDTLRDTLEERNA---TV 63
<del>::</del> ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AKLELRSAQKDLQSADQEITSLRKKSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEDEQALANRLTRQSKENAQRIIEIEDELEHER-QSRSKADRARAELQRELDELNERLDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEEAVEREKRIRAETEKSKRKVEGELKGAQETIDELSAIKLETDASLKKKEADIHALGVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IELLLQSQ----RSEVEEMIR----DMGVGQSAVEQLAVYCV----SLKKEYENL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSLQDEMNSQDETIGKINKEKKLLEENNRQLVDDLQAEEAKQA--QANRLRGKLEQTLDE 1040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESLQNALNKAEMLCSTLKKQMKFLEQ-------RQDETKQAREEAHRLKCKM-KTMEQ 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKSLNDANDRLSEHEEKNADLEKQRRKAQQEVENLKKSIEAVDGNLAKSLEEKAAKENQI
                                              Similarity 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                          984
1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 40, Last annotation update)
t modulatory factor (TMF).
                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human).
etazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
theria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                          1092
                                                                                                                                                                                                                                                              ormatics Institute. There are no rest
institutions as long as its content
tatement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -KEARKATGELADRLKKDLVSSRSK----
                                                           14.2%;
                                                                                                                       Lion; DNA-binding; Repressor; Coiled
22 COILED COIL (POTENTIAL).
92 COILED COIL (POTENTIAL).
123170 MW; 26133E8E5F4677BE CRC64;
···
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.3%;
                                              49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56;
                                             Score 153; DB
Pred. No. 0.11;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 153.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .19;
                                                                          ۳.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sparkes R.S., Gaynor R immunodeficiency virus
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                                         99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82;
                                                                          Length 1093;
                                                                                                                                                                     Coiled
                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                     coil
                                             34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67;
                                                                                                                                                                                                                                                                                                                                                                        INHIBITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 982
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                                                                                                                                                                                                                                                                                                                                                                                                                     .B.;
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RESULT 25
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             EMBL;
HSSP;
                                       EMBL;
                                                                                                                                                                                                                 modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                    "The human extraocular muscle myosin heavy chain gene the cluster of fast and developmental myosin genes on Genomics 54:188-189(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99318869; PubMed=10388558; Weiss A., Schiaffino S., Leinwand L.A.; Comparative sequence analysis of the complete human sarcomeric myosin heavy chain family: implications for functional diversity."; 12. Mol. Biol. 290:61-75(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYHD_HUMAN
Q9UKX3; 09
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Extraocular muscle; MEDLINE=99026150; PubMed=9806854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, skeletal muscle, extraocular (MyHC-eo)
                                                                                                                                                                                                                                                                                                                                                                                                                                              Winters L.M., Briggs M.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Extraocular muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1917-1938 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       501
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89
                                                                                                                                                                              SIMILARITY: CONTAINS 1 MYOSIN-LIKE SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                        MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (H) SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS SUBFRAGMENT (S2).
                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MUSCLE CONTRACTION
           AF111782; AAD:
AF075248; AAC:
P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKQHRENIKKLNSMVERQEKDLGRLQVDMDELEEKNRSIQAALDSAYKELTDLHK 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKATGELADRLKKDLVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EAHRLKCKMKTMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFTQRIAEAEKKVQLACKERDAAKKEIKNIKEELATRLNSSETADLLKEKDEQIRGLME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGEKLSKQQLHNSNIIKKLRAKDKENENMVAKL---NKKVKELEEELQHLKQVLDGKEEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              095252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                          AAD29948.1; -. AAC83241.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schachat F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1938
                                                                                                                                                                                             GLOBULAR HEAD DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                http://www.isb-sib.ch/announce/
                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                    (MYH13) maps t chromosome 17.
                                                                                               and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159
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603487;

InterPro;

IPR004009; IPR002928; IPR000048;

Myosin_N. Į.

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В
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STRAIN-BRISTOL N2;

K MEDLINE-89178677; PubMed-2926820;

A Dibb N.J., Maruyama I.N., Krause M., Karn J.;

A Dibb N.J., Maruyama I.N., Krause M., Karn J.;

T "Sequence analysis of the complete Caenorhabditis ele
T heavy chain gene family,";

Theavy chain gene family,";

RL J. Mol. Biol. 205:603-613(1989).

CC -!- SUBUNIT: MUSCLE CONTRACTION.

CC -!- SUBUNIT: MUSCLE CONTRACTION.

CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THE CONTRACTION.

CC -!- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THE CONTRACTION.
                                                                                                                                                                                                                                                                                                                                                               δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Вb
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Best Local S
Matches 59
                                                                                                                                                                                                                                        MYSA_CAEEL
P12844;
01-OCT-1989
01-OCT-1989
                                                                                                                                                                                                                                                                                           _CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART;
SMART;
                                                                                                                                                                                                                                                                                                                                             1541
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MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pfam; PE00063; myosin_head; 1.
pfam; PF02736; myosin_n; 1.
pfam; PF01576; myosin_tall; 1.
pfam; PF01576; myosin_tall; 1.
prINTS; PR00193; mYOSINHEAVY.
PTODOM; PD000355; myosin_head;
SMART. SMO015
                                                                                                                                                                  Eukaryota; Metazoa;
Rhabditidae; Pelode
                                                                                                                                                                                        Caenorhabditis elegans
                                                                                                                                                                                                                 Myosin
                                                                                                                                                                                                                                                                                                                                                                                            1502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50096; IQ; 1.
Myosin; Muscle protein; Coiled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                        MYO-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Calmodulin-binding;
                                                                                                                                                                                                                              16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                      NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                    117
                                                                                                                                                                                                                                                                                                                                                                   171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 DAEFLKNELDSVKAQLSQKDREKRDSQAIID ---- TLRDTLEERNATVESLQNALNKAEM 75
                                                                                                                                                                                                                                                                                                                                         KSDLQVALEEVEGSLEHEESKILRVQLELSQVKSEL---DRKVIEKDEEIEQLKRNS
                                                                                                                                                                                                                                                                                                                                                                                          LRRENKNLQEEISDLTEQIAETG----
                                                                                                                                                                                                                                                                                                                                                                                                       ACATLDKKQRNFDKVLAEWKQKLDESQAELEAAQKESRSLSTELFKMRNAYEEVVDQLET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCSTL-KKQMKF------LEQRQDETKQAREEAHRLKCKM-----KTMEQIEL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DAIQRTEELEEAKKKLAQRLQEAEEKTETANSKCASLEKTKQRLQGEVEDLMRDLERSHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PF00612; IQ; 2.
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SM00242; MYSc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001609;
                                                                                                                                                                                                                 (Rel. 12, Created)
(Rel. 12, Last sequence update)
(Rel. 40, Last annotation updat
y chain A (MHC A).
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843
179
659
761
130
                                                                                                                                                                  Peloderinae;
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1938

1938

186

681

775

130

699

709

709

723678 1
                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                  LVSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATP-binding;
                                                                                                                                                                 Nematoda; Chromadorea;
inae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Myosin_tail.myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP (POTENTIAL).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

ACTIN-BINDING (BY SIMILARITY).

METHYLATION (TRI-) (POTENTIAL).

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

BUKYLATION (SH-2) (POTENTIAL).

MW; 1F6D006416381CD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 153; DB Pred. No. 0.2; 40; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQ.
COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coil; Thick filament; Actin-binding
               HEXAMERIC PROTEIN THAT CONSISTS OF 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methylation;
                                                                                                                                                                                                                                                                               1969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEAD-LIKE
                                                                                                                                                                                                                             update]
                                                                                                                                                                                                                                                                               Ā
                                                                                                                                                                                                                                                                                                                                                                                          -----KNLQEAEK-TKKLVEQE
                                                                                                                                                                             Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alkylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1938
                                                                             elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                            myosin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                  216
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Best Local S
Matches 62
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

- I SUBCELLULAR LOCATION: Thick filaments of the myofibrils.
- I DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
- I PTM: TWO CYSTEINE RESIDUES IN THE SI DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY.
- I MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

- MISCELLANEOUS: THERE ARE FOUR DIFFERENT MYOSIN HEAVY CHAINS IN C. ELEGANS.
                                                                                                                                                                                                                                                                               MOD_RES
MOD_RES
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                              Myosin; Muscl
ATP-binding;
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Pfam; PF00063; myosin_head; 1.
Pfam; PF02736; myosin_N; 1.
Pfam; PF01576; myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X08067; CAA30856.1; PIR; S02771; S02771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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InterPro; IPR001609;
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InterPro; IPR004009;
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 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - EDUTOPEAN BIOINFORMATICS INSTITUTE. There are no restrictions on its by non-profit institutions as long as its content is in no way
 LKKEYENLKEARKATGELADRLKK---DLVSSRSKLKTLNT---ELDQAKLELRSAQKDL
                             SNRKLNEDLQSEEDKVNHLEKIRNKLEQQMDELEENIDREKRSRGDIEKAKRKVE---GD
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SM00015; IQ; 1.
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ATP.
ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).

MW; 64577BBAF7EADBOA CRC64;
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Pred. No. 0.23
47; Mismatches
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_HUMAN HIP1_HUMAN STANDARD; PRT; 995 AA. 000291; 000328; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Huntingtin interacting protein 1 (HIP-I) (Fragment).
                                                                                                                                                                                                              ALTERNATIVE SPLICING.
MEDLING-20519263; PubMed-11063258;
Chopra V.S., Metzler M., Rasper D.M.,
Singaraja R., Gan L., Fichter K.M., M.
Nicholson D.W., Hayden M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97285121; PubMed=9140394; K., Graham R.K., Nicho Kalchman M.A., Kolde H.B., McCutcheon K., Graham R.K., Nicho Nishiyama K., Kazemi-Esfarjani P., Lynn F.C., Wellington C., Nishiyama K., Kazemi-Esfarjani P., Lynn F.C., Wellington C., Metzler M., Goldberg Y.P., Kanazawa I., Geitz R.D., Hayden M., Goldberg Y.P., Kanazawa I., Geitz R.D., Hayden M., HIPI, a human homologue of S. cerevisiae Slažp, interacts w membrane-associated huntingtin in the brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hug A.H.M.M., Nichol K., Hayden M.R.;
"Genomic organization of
                                                                                                                                                           "HIP12 is a non-proapoptotic member of a nan interacting protein with huntingtin."; Mamm. Genome 11:1006-1015 (2000).
-i- FUNCTION: MAY PLAY A FUNCTIONAL ROLE
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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            IN BRAIN.
MISCELLANGUS: THE AFFINITY OF THE HUNTINGTIN PROTEIN-HIP1
INTERACTION IS INVERSELY CORRELATED TO THE LENGHT OF THE
INTERACTION IS INVERSELY OF THE HUNTINGTIN PROTEIN IN HUN
                                                               SUBCELLULAR LOCATION: CYTOPLASMIC.
ALTERNATIVE PROBUCTS: 2 ISOFORMS;
BY ALTERNATIVE SPLICING.
BY ALTERNATIVE SPLICING.
 POLYGLUTAMINE DISEASE.
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                                                                                                                                                                                                                                                                                                        E.E., Rovira C., Scherzinge
b., Colicelli J., Lehrach H.;
a huntingtin interacting p
system.";
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Pfam; PF01417; ENTH; 1.
Pfam; PF01608; I_LWEQ; 1.
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{\tt TQEQLE-VLESLKQELATSQRELQVLQGSLETSAQSEANWAAEFAELEKERDSLVSGAAH}
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RA50_PYRAB
                                                                                                                                                                                                                                                             NP_BIND
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                         "Pyrococcus abyssi genome sequence: insights into archaeal structure and evolution."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the
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                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003593;
InterPro; IPR003439;
InterPro; IPR001687;
                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ248286; CAB50131.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: Forms a complex with mrell (By similarity). SIMILARITY: BELONGS TO THE SMC FAMILY. RAD50 SUBFAMILY.
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Pred. No. 0.
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MYSP_CAEEL
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01-JUL-1989
15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
Eukaryota; Metazoa; Nem
Rhabditidae; Peloderina
                                                                                                                                                                                                                                                      -!- SUBCULULAR LOCATION: Thick filaments of the myofibrils
-!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils
-!- DOMAIN: FOR MOST OF ITS LENGTH, PARAMYOSIN APPEARS TO FORM AN ALPHA-HELICAL COLLED COIL AND SHOWS THE HEPPAD REPEAT OF HYDROPHOBIC AMINO ACID RESIDUES AND THE 28-RESIDUE REPEAT OF CHARGED AMINO ACIDS CHARACTERISTIC OF MYOSIN HAVING CHAINS. HOWEVER, PARAMYOSIN DIFFERS FROM MYOSIN IN HAVING NON-HELICAL EXTENSIONS AT BOTH TERMINI AND AN ADDITIONAL "SKIP" RESIDUE THISTERRUPTS THE 28-RESIDUE REPEAT. THE DISTRIBUTION OF CHARGED RESIDUES IS ALSO DIFFERENT FROM MYOSIN HEAVY CHAINS.
                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89329036; PubMed=2754733; Schriefer L.A., Waterson R.H.; "Phosphorylation of the N-terminal region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kagawa H., Gel
J. Mol. Biol.
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                s04027; s
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                                                                                                                                   European Bioinformatics Institute.
                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
by non-profit institutions as long as its content is in
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P80220;
                                                                  an email to license@isb-sib.ch).
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                                                                                    requires a
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1. 211:665-665(1990).
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(Rel.
(Rel.
                S04027.
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Last annotation update)
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                                                                                  agreement (see http://www
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PF01576; Myosin_tail;

IPR002928; Myosin_tail.

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                                                                                                                                                TISSUE-Testis;

MEDLINE-98037449; PubMed-9371398;

KONGOh N., Nishina Y., Tsuchida J., Koga M., Tanaka H.,

Inazawa J., Taketo M., Nozaki M., Nojima H., Matsumiya

Okuyama A., Nishimune Y.;

"Assignment of synaptonemal complex protein 1 (SCP1) to the synaptonemal stup hybridization
chromosome 1p13 by fluorescence in situ hybridiz
expression in the testis.";
Cytogenet. Cell Genet. 78:103-104(1997).
-1- FUNCTION: MAJOR COMPONENT OF THE TRANSVERSE
SYNAPTONEMAL COMPLEXES (SCS), FORMED BETWEEN
CHROMOSOMES DURING MEIOTIC PROPHASE.
-1- SUBCELLGUAR LOCATION: NUCLEAR. IN TRIPARTITE
SYNAPTONEMAL COMPLEXES, BETWEEN LATERAL ELEM
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Meuwissen R.L.J.,
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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NONHELICAL REGION (POTENTIAL).
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Matsumiya K., Nam
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TISSUE SPECIFICITY: TESTIS.
DOMAIN: CONSISTS OF AN ALPHA-HELICAL STRETCH OF
FLANKED BY N- AND C-TERMINAL GLOBULAR DOMAINS.
DOMAIN HAS DNA-BINDING CAPACITY (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FOUND ONLY WHERE THE CHROMOSOME CORES ARE SYNAPSED. ITS FOUND TOWARDS THE CENTRE OF THE SYNAPTONEMAL COMPLEX C-TERMINUS EXTENDS WELL INTO THE LATERAL DOMAIN OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collal een the Swiss Institute of Bioinformatics and the EMBL outs European Bioinformatics Institute. There are no restrictions
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RESULT 31
MYH8_HUMAN
     RA ESSET K., Tidhar A., Myszkowski M.;

RA ESSET K., Tidhar A., Myszkowski M.;

RI Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.

CI := FUNCTION: MUSCLE CONTRACTION.

CC -!- FUNCTION: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

CC HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

CC AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

CC -!- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

CC -!- SUBCELLULAR FORTICLE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CC -!- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CC CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,

CC CYCLES OF A 28-RESIDUES IN THE SIDOMAIN ARE SELECTIVELY

CC --- PTM: TWO CYSTEINE RESIDUES IN THE SIDOMAIN ARE SELECTIVELY

CC --- PTM: TWO CYSTEINE RESIDUES IN THE SIDOMAIN ARE SELECTIVELY

CC --- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT

CC MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE

CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRACMENTS (S1) AND 1 ROD-SHAPED

CC SPLIT FURTHER INTO 2 GLOBULAR SUBFRACMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYH8_HUMAN STANDARD; PKT; 19
P13535; Q14910;
D1-JAN-1990 (Rel. 13, Created)
15-JUL-1998 (Rel. 36, Last sequence up
16-OCT-2001 (Rel. 40, Last annotation
     use by modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            myosin
Eur. J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-Skeletal muscle;
TISSUE-Skeletal muscle;
MEDLINE-9023631; PubMed-2373371;
MEDLINE-9023631; PubMed-2373371;
Rersch-Mizrachi I., Feghali R., Shows T.B. Jr., Leinwand L.A.;
"Generation of a full-length human perinatal myosin heavy-chain-encoding cDNA.";
encoding cDNA.";
Gene 89:289-294(1990).
              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-46 FROM N.A. Esser K., Tidhar A., Myszk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 860-1937 FROM N.A. MEDLINE-89234168; PubMed-2715179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Characterization of transcript.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Skeletal muscle;
MEDLINE=95324556; PubMed=7601129;
MEDLINE E.H., Kelly A.M., Pompido
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Feghali R., Leinwand L.A.;
"Molecular genetic characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification of three developmentally controlled isoforms of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                      MEROMYOSIN (LMM) AND 1 HEAVY N
SPLIT FURTHER INTO 2 GLOBULAR
SUBFRAGMENT (S2).
SIMILARITY: CONTAINS 1 MYOSIN-
SIMILARITY: CONTAINS 1 IQ DOM/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     perinatal myosin heavy chain.";
Ll Biol. 108:1791-1797(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Buchberger-Seidl A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chains
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Rubinstein N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               muscle
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Primates;
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                                                                                                        MYOSIN-LIKE GLOBULAR IQ DOMAIN.
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   removed.
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on update)
, perinatal (MyHC-perinatal).
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Usage
                                                                                                                        HEAD
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Best Local 9
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Pfam; PF02736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfanr; PF01576; Myosin_tail; 1.
PRINTS; PR001935; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM00044; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
SEQUENCE
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MOD_RES
CONFLICT
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   1499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myosin; Muscle protein; C ATP-binding; Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A30220; A30220.
HSSP; P08799; 1LVK.
                                                                                                                                                                                                                                                           1272 LINDL---TAQRARLQTEAGEYSRQLDEKDALVSQLSRSKQASTQQIEELKHQLEEETKA 1328
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Pfam; PF00612;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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 ETLRRENKNLQ---
                              E-LRSAQKDLQSADQEITSLRKK
                                                              NAACAALDKKQRNFDKVLSEWKQKYEETQAELEASQKESRSLSTELFKVKNVYEESLDQL 1498
                                                                                                                                               TKQAREE-AHRLK-------CKMKTMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQL 142:::::: | | |::: | |::: | |::: |
                                                                                                                                                                                           KNALAHALQSSRHDCDLLREQYEEEQEGKAELQRALSKANSEVAQWRTKYETDAIQRTEE
                                                                                                                                                                                                                             VESLQNALNKAEMLCSTLKKQMKFLE---
                                                                                             AVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKLKTLNTELDQAK--
                                                                                                                             LEEAKKKLAQRLQEAEEHVEAVNAKCASLEKTKQRLQ---NEVEDLMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M36769; AAC17185.1; -.
                                                                                                                                                                                                                                                                                                                            Similarity 24.0
64; Conservative
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IPR002928;
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·QEISDLTEQ 1518
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24.3%;
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Myosin_tail.
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                                                                                                                                                                                                                                                                                                                                                                                                     METHYLATION (SH-1) (POTENTIAL).
ALKYLATION (SH-2) (POTENTIAL).
A -> R (IN REF. 2).
E -> Q (IN REF. 1 AND 4).
M -> N (IN REF. 3).
N -> H (IN REF. 1 AND 4).
MC -> DGG (IN REF. 3).
E -> G (IN REF. 1 AND 4).
KY -> NT (IN REF. 3).
KY -> NT (IN REF. 3).
E -> D (IN REF. 1 AND 4).
KY -> NT (IN REF. 3).
E -> D (IN REF. 1 AND 4).
C -> DGIN REF. 1 AND 4
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18; Mismatches
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COILED
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THE RESERVE AND DESCRIPTION OF THE PROPERTY OF
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                                                                                             Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
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Pfam; PF01576; Myosin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Choi O.H., Park C., Itoh K., Adelstein R.S., Beaven M.A.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CELLULAR MYOSIN APPEARS TO PLAY A ROLE IN CYTO
CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain, type A) (Nonmuscle myosin heavy chain-A) (NMMHC-A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAT
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InterPro; IPR001609;
Pfam; PF00612; IQ; 1.
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                         ΝP
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                                                                                                                                                                                           SEQUENCE
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                      10 DLAQEEENVL --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CELL SHAPE, AND SPECIALIZED FUNCTIONS SUCH AS SECRETION CAPPING.
CAPPING.
SUBUNIT: MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (ML REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, CYCLES OF A 28 RESIDUE REPEAT PATTERN COMPOSED OF 4 HEP CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way iffied and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00063; myosin_head; 1.
                                                                       l Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                    coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00242;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00015;
                                                                                                                                                                                                                                                                                                                                                                                       ATP-binding; Calmodulin-binding; coil; Alkylation; Multigene family
                                                                                                                                                                                                                                     ; Alkylation; Multigene f.
1 778 MYOSIN 1
779 808 IQ.
841 1927 COILED (
174 181 ACTIN-B (
654 654 ALKYLAT
                                                                       Conservative
  <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYSc;
                                                                                                                                                                                           A,
-DAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myosin_tail.
myosin_head.
                                                                                             14.0%;
25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myosin_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                           226336
                                                                                                                        IQ.

COILED COIL (PULD...
ATP (POTENTIAL).

ACTIN-BINDING.

ALKYLATION (SH-1) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

ALKYLATION (SH-2) (POTENTIAL).

ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .,
                                                                       44;
                                                                                           Score 150;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                            MYOSIN HEAD-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1961
                                                                                           DB
. 29;
                                                                                                                                                                                                                                                                                                                                                                                                        Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ã
                                                                                                                 1;
                                                                  96;
                                                                                                                    Length 1961
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S OF 2
(MLC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEPTAPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOKINESIS
                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHOWING
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AND 2
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                                                                     Gaps
                        65
                                                                     7;
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RESULT 33
MYSS_CYPCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вb
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                                                                                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hirayama Y. Watabe S.;

**Structural differences in the crossbridge head of temperature-

**The content of the crossbridge head of temperature-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cypriniformes; Cyprinidae; Cyprinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acclimation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      muscle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  muscle."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Fast muscle;
MEDLINE=97352533; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyprinus carpio (Common carp).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Myosin heavy chain, fast skeletal muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q90339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYSS_CYPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1402 LEEKVAAYDKLEKTKTRLQQ----ELDDLLVDLDHQRQSVSNLEKK 1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1228 ELANEVKALLQGKGDSEHKRKK---VEAQLQELQVKFSEGERVRTELADKVSKLQVELDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Watabe S., Imai J., Nakaya M., Hirayama Y., Uozumi T., Hirono I., Aoki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95194396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1387-1528 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97176447; PubMed=9023993;
Imai J., Hirayama Y., Kikuchi K., Kakinuma M., Watabe S.;
"cDNA cloning of myosin heavy chain isoforms from carp fast skeletal muscle and their gene expression associated with temperature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eur. J. Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7962;
                                                                      SUBFRAGMENT
- SIMILARITY:
- SIMILARITY:
                                                                                                                                             PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALKYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY. MISCELLANBOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
SWISS-PROT entry
een the Swiss Ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LEEEEEEAKRNL--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQNALNKAEMLCSTLKKQMKFLEQRQDETKQAREEAHR-----LKCKMKTMEQIELLLQSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSSRSKLKTLNTELDQAKLELRSAQKDLQSADQEITSLRKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           981-1935 FROM
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                                                                                                                          (82)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                      CONTAINS 1 MYOSIN-LIKE CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                246:380-387(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=7887920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=9208928;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -EKQIATLHAQVTDMKKKMEDGVGCLETAEEAKRRLQKDLEGLSQR 1401
                    is copyright.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
ght. It is produ
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                                                                                                   GLOBULAR HEAD DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata;
Euteleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                    produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Okamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Υ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ostariophysi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 skeletal
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Best Local 9
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Pfam; PF00613; IQ; 1.
Pfam; PF002736; Myosin_head; 1.
Pfam; PF02736; Myosin_tail; 1.
Pfam; PF01576; Myosin_tail; 1.
Pfam; PF01576; Myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
Pr0Dom; PD000355; Myosin_head; 1.
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
NP_BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
Pfam; PF0
MYH9_HUMAN STANDARD; PRT; 1960 AA.
P35579; O60805;
O1-JUN-1994 (Rel. 29, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
O1-MAR-2002 (Rel. 41, Last annotation update)
MYOSIn heavy chain, nonmuscle type A (Cellular myosin heavy chain,
                                                                                         HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
MOD_RES
MOD_RES
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
EMBL;
                                                                                                                                                1792
                                                                                                                                                                                                                                                     1672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                         1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                           154
                                                                                                                                                                                                                                                                                                                                 62
                                                                                                                                                                                                                                                                                                                                                                                  11 LAQEEENVLDAEFLKNELDS-VKAQLSQKDRE----KRDSQAIIDTLRDTLE----ERNA
                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; D89992; BAA22069.1; -
; D50476; BAA09069.1; -
; D43700; BAA07802.1; -
; P08799; LMMD.
                                                                                                                                                                                                                                                                                                                      TV---ESLQNALNKAEMLCSTLKKQ----MKFLEQRQDETKQAR---EEAHR----LKCK
                                                                                                                                              KDLQHRLDEAESLAMKGGKKQLQKLESRVREL 1823
                                                                                                                                                                                                                                                  VAMVERRNSLMQAEIEELRAALEQTERGRKVAEQELVDASERVGLLHSQNTSLINTKKKL
                                                                                                                                                                                                                                                                                                     ALRVKKKMEGDLNEMEIQLSHANRQAAEAQKQLRNVQGQLKDAQLHLDEAVRGQEDMKEQ
                                                                                                                                                                                                                                                                                                                                                         LEHEESKILRVQLELNQVKSEIDRKLAEKDEEMEQIKRNSQRVIDSMQSTLDSEVRSRND
                                                                                                                                                                       KTLNTELDQAK-LELRSAQKDLQSADQEITSL
                                                                                                                                                                                                EADLVQVQGEVDDAVQEARNAEEKAKKAITDAAMMAEELKKEQDTSAHLERMKKNLEVTV
                                                                                                                                                                                                                                                                              MKTMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000048; IQ.
IPR004009; Myosin_N.
IPR002928; Myosin_tail.
IPR001509; Myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           family.
                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781
811
839
1935
185
681
775
129
                                                                                                                                                                                                                        ·NLKEARKA······TGELADRLKKDLVSS····RSK····-L
                                                                                                                                                                                                                                                                                                                                                                                                                        13.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               221599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alkylation; Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COILED COIL (POTE ATP (POTENTIAL). ACTIN-BINDING. ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 149; DB
Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HINGE
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                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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RA Blakey S., Bridgeman A.M., Buck N., Beasley O., Bird C.F.,
RA Blakey S., Bridgeman A.M., Buck D., Burgess J., Burrill W.D.,
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Cornoy D., Corby N.
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Cornoy D., Corby N.
RA Cobley V., Cole C.G., Collier R.E., Connor R.E., Cornoy D., Corby N.
RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dockree C.,
RA Coville G.J., Cox A.V., Davis J., Cox A.V., Hall R., Hall-Tanlyn G.,
RA Kimberley A., King A., Laird G.K., Langford C.F., Leversha M.A.,
RA Milne S.A., Mortimore B.J., Hall C.N., Mashreghi-Mohammadi M.,
RA Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA Pearson D., Phillimore B.J., Odell C.N., Pavitt R., Pearce A.V.,
RA Pearson D., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Milner T.E., Wilning L., Wright C.L., Hubbard T., Bentley D.R.,
RA Wilteley M.N., Willey D., Williams L., Williams S., Milliamson H.,
RA Mitsuyama S., Roe B.A., Chen F., Chu L., Crabiree J., Deschamps S.,
RA Mathyama S., Roe B.A., Chen F., Chu L., Crabiree J., Deschamps S.,
RA Muyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S.,
RA Milner T., Scham M., Zhang G., Chissoe S., Murtay J., Miller M.,
RA Milner S., Cordes M., Johnson D., Bemis G., Bentley D., Bradshaw H.,
RA Milner S., Chan M., Zhang G., Chissoe S., Murtay J., Miller M.,
RA Milner S., Chan M., Zhang G., Chissoe S., Murtay J., Miller M.,
RA Milner S., Schett P., Walker C., Wamsley A., Wohldmann P., Pepin K.,
RA Milner S., Shakh T., Kurahashi H., Saitta S.,
RA Milner S., Williams D., Sarous E., Fransson I., Tapia I., Bruder C.E.,
RA Milner S., Williams D., Shaull E., Shizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20057165; PubMed=10591208;
Dunham I., Hunt A.R., Collins J.E., Bruskiewich R., Beare D.M. Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A., Clamp M., Smink L.J., Barlow K., Bates K.N., Beasley O., Bi
                                                                                                                                                                                                                                                                                                       Toothaker L.E., Gonzalez D.A., Tung N., Lemons R.S., le Beau M.M. Arnaout M.A., Clayton L.K., Tenen D.G.;
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Simons M., Wang M., McBride O.W., Kawamoto S., Yamakawa
Gdula D., Adelstein R.S., Weir L.;
"Human nonmuscle myosin heavy chains are encoded by two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                  Circ.
                                                                                                                                                         on different chromosomes.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature
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CAPPING:
CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC) AND 2
REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

POMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING
CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
CHARACTERISTIC FOR ALPHA-HELICAL COILED COILE.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

CHARACTERISTIC FOR ALPHA-HELICAL COILED COFFECTIVE SYNDROME (FTOS), AN AUTOSOMAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.

WITH ADDITIONAL ALPORT LIKE CLINICAL FEATURES OF SENSORINEURAL DEAFNESS, CATARACTS AND NEPHATIS.

CIBSS) AN AUTOSOMAL DOMINANT MACROTHROMBOCYTOPENIA CHARACTERIZED BY THROMBOCYTOPENIA, GIANT PLATELETS AND LEUKOCYTE INCLUSIONS.

CHARACTERIZED BY PROGRESSIVE HEARING INFORMAL DOMINANT CHARACTERIZED BY ROORSESSIVE HEARING INFORMAL DOMINANT CHARACTERIZED BY PROGRESSIVE HEARING INFORMAL DOMINANT AND COCHLEOSACCULAR DEGENERATION.

COCHLEOSACCULAR DEGENERATION.

COCHLEOSACCULAR DEGENERATION.

COCHLEOSACCULAR DEGENERATION.
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May Hegglin anomaly.",
Nat. Genet. 26:106-108(2000).

-i- FUNCTION: CELLULAR MYOSIN APPEARS TO P
-i- FUNCTIONS
AND SPECIALIZED FUNCTIONS
                                                                                                                   EMBL;
EMBL;
EMBL;
EMBL;
HSSP;
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                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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[7]
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Nat. Genet. 26:103-105(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mutation of MYH9, encoding non-muscle
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MEDLINE=20428193; PubMed=10973260;
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Lalwani A.K., Goldstein J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Mutations in MYH9 result in the May-Hegglin anomaly, and Fechtner and
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                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its
                                                                                                                 282215; CABO5105.1; -...; M81105; AAA59888.1; -...; M69180; AAA61765.1; -...; M31013; AAA538349.1; -...; P08799; 1LVK.
                                                                                               160775;
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IPR000048;
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Best Local Similarity
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Coiled coil;
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                                                                        182
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InterPro; IPR002928;
InterPro; IPR002017;
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KKSDD
                                  QDTQELLQEENRQKLSLSTKLKQVEDEKNSFREQLEEEEEAKHNLEKQIATLHAQVADMK
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                                                                                                                                               EEMIRDMGV---
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PF02736; Myosin_N; 1.
PF01576; Myosin_tail; 1.
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Myosin_tail.
Spectrin.
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19.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Calmodulin-binding; Actin-binding;
ion; Multigene family; Disease mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        myosin_head
                                                                                                                                                                                                                                                                                                                                                                                                         68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KG -> GR (IN REF. 4).
E -> EE (IN REF. 2).
T -> A (IN REF. 2).
S -> G (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAI -> RGH (IN REF. T -> S (IN REF. 3).
T -> M (IN REF. 4).
C -> Y (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E -> K (IN MHA).
/FTId=VAR_010797.
EAI -> RGH (IN RE
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R -> C (IN SBS).
/FTId=VAR_010795.
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 149;
Pred. No. 0.
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                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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(SH-2) (POTENTIAL).
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WYHB_CHICK
ID MASSAL
AC P10587.
DT 10-JUL
DT 15-DEC
DT 16-DEC
DT 1
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Masaki T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain deduced from its complementary DNA sequence.
topography and function of myosin.";
J. Mol. Biol. 198:143-157(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Myosin heavy chain, gizzard smooth muscle. Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vert Archosauria; Aves; Neognathae; Galliformes;
                                                                                                         use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pre-power stroke state.";
Cell 94:559-571(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dominguez R., Freyzon Y., Trybus K.M., Cohen C.; "Crystal structure of a vertebrate smooth muscle myosin motor and its complex with the essential light chain: visualization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maita T., Onishi H., Yajima E., Matsuda G.; "Amino acid sequence of the amino-terminal heavy chain of chicken gizzard myosin."; J. Biochem. 102:133-145(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation muscle.
                                                    EMBL; X06546; CAA29793.1;
                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98412652; PubMed=9741621;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-88032919; PubMed=3312184; Maita T., Onishi H., Yajima E., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Masaki T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=88118918; PubMed=2892941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete primary structure of vertebrate smooth muscle myosin heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yanagisawa M., Hamada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PARTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

PTM: TWO CYSTEINE RESIDUES IN THE S1 DOMAIN ARE SELECTIVELY ALXYLATED AND ARE REQUIRED FOR MYOSIN ATPASE ACTIVITY MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED
                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                         SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2). SUBCELLULAR LOCATION: Thick filaments of the myofibrils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: MUSCLE CONTRACTION.
SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF
HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)
                                                                                                                                                                                                                                                                                                                                                                                                 SUBFRAGMENT (S2)
                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKMED
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                                                                                                                                    (See http://www.isb-sib.ch/announce/
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mes; Phasianidae; Phasianinae;
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InterPro; IPR002017; Spectrin
InterPro; IPR001600
                                                                                                                                                                 01-JUN-1994 (Rel. 2
15-JUL-1998 (Rel. 3
Myosin heavy chain,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC;
PROSITE; PS50096; IQ;
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                                                                                                                                                                                                               01-JUN-1994
01-JUN-1994
                                                                                                                                                                                                                                                         MYSU_RABIT
Q99105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1002
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Pfam; PF01576; MyOsin_tail; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
    MEDLINE=91139672;
                        SEQUENCE FROM
TISSUE=Fetal a
                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                Oryctolagus cuniculus (Rabbit).
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Pfam; PF00612; IQ; 1
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                        aorta;
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                                                                                                                                                                                     29, Created)
29, Last sequence update)
36, Last annotation updat
    PubMed=1995631;
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                                                                                                                                                                        embryonic smooth muscle
                                                                                                        Lagomorpha;
                                                                                                                              Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 149; DB 1; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MISSING (IN REF. 3).
KDTSITQGPSFS -> RTPASLKVHLFP (IN B7B6C923E5273D93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHYLATION (TRI-) (POTENTIAL).
ALKYLATION (SH-1).
ALKYLATION (SH-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTIN-BINDING BLOCKED.
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                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                      Leporidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COIL
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                                                                                                                                                                                         update)
                                                                                                                              Vertebrata;
                                                                                                                                                                                                                                                                            ΑA
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                                                                                                        Oryctolagus
                                                                                                                                                                   isoform (Fragment).
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                                                                                                                              Euteleostomi;
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Best Local
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                 MFP1_ARATH STAI
Q9LW85;
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
MAR binding filamen
MFP1 OR AT3G16000 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - I- SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

- I- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

- I- DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES, CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

- I- MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S2).

- I- SIMILARITY: THE PERIODICITIES OF HYDROPHOBIC AND CHARGED RESIDUES, WHICH DICTATE THE ALPHA-HELICAL COILED-COIL STRUCTURE ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002928; myosin_tail.
Pfam; PF01576; myosin_tail; 1.
myosin; muscle protein; Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - -
    Arabidopsis
                                                                                                                                                                      ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires
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arteriosclerosis.":
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"cDNA cloning of a myosin heavy chain isoform in embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kuro-0 M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: MUSCLE CONTRACTION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEEENVLDAEFLKNELDSVKAQLSQKDREKRDSQAIIDTLRDTLEERNATVESLQNALNK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A38650;
                                                                                                                                                                                                                                                                                                                                    DLKDLEAQIEAANK---ARERRVKQLRRLQAQMKDYQRELEEARGSRDEIFAQSKE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEMLCSTLKKQMKFLEQRQDE-----TKQAREEAHRLKCKMK----TMEQIEL 116
                                                                                                                                                                                                                                                    SEKKLKSLEAEILQLQEELASSERARRHAEQE
                                                                                                                                                                                                                                                                                             SRSKLKTLNTELDQAKLELRSAQKDLQSADQE
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                                                                                                                                                                                                                                                                                                                                                                              LLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVS
                                                                                                                                                                                                                                                                                                                                                                                                                         LEVNTQAMKAQFERDLQARDEQSEEKKRLLTKQVRELEAELEDERKQRALAVASKKKMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D10280; BAA01124.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nagai R.,
    (Rel. 40, Createu, (Rel. 40, Last sequence update) (Rel. 40, Last annotation updat filament-like protein 1. 3G16000 OR MSL1.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                   STANDARD;
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457
58118 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49;
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COILED COIL (POTENTIAL).
; 49F793247D00973E CRC64;
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Pred. No. 0.
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SEQUENCE
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"Structural analy features of the r clones.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosiceurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB012247; BAB02666.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20277480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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ROS. 8:131-135(2000).

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                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pean Bioinformatics Institute. There are no rest non-profit institutions as long as its content
                                                                                                                                                                                                                                           727
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                                                                                                                                                                                                                                                                                                                                          140
     Conservative
                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                  DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10819329;
                                                                                                                                                                                                                                                                                                                                          692
                                                                                                                                                                                                                                           35 F
82071 MW;
                                        13.8%;
     53;
                                   Score 148.5; D
Pred. No. 0.13;
                                                                                                                                                                                                                                           POLY-SER.
5F4F9A0F7F623CAA CRC64;
                                                                                                                                                                                                                                                                                                                                COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                  Coiled coil.
     Mismatches
                                                                                               DB 1;
     84;
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     Indels
                                                                                     Length
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I. Sequence
61;
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Gaps
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01-OCT-1996 (Rel.
01-OCT-1996 (Rel.
15-JUL-1998 (Rel.
              Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Me
                                                                                                                        P50532;
01-OCT-1996
Xenopodinae;
                                              Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                  KDKVADLTEKYED
                                                                           assembly protein
                                                                                                                                                        STANDARD;
                                                                                        34, Created)
34, Last sequence update)
36, Last annotation updat
                ); Craniata; Ve
Mesobatrachia;
                                                                             XCAP.
                                                                                                                                                        PRT;
                                                                                                                                                        1290
                                                                                           update)
                Vertebrata;
ia; Pipoidea;
                                                                                                                                                        B
                Euteleostomi;
; Pipidae;
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----ARKATGELADRLKKDLVSSR-SKLKTLNTELDQAKLELRSAQKDLQSA

-ALDDVNKS

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218

-KTMEQIELLLQSQRSEVEEMIRDMGVGQSAVEQLAVYCVSLKKEYENL 156

EMLCSTLKKQMKFLEQRQD-----ETKQAREEAHRLKCKM-----

108

65

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RESULT 39
REST_HUMAN
ID REST_HUMAN
AC P30622;
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Best Local
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NP_BIND 107 114

DOMAIN 264 594

DOMAIN 764 1027

DOMAIN 1094 1129

DOMAIN 1263 1290

DOMAIN 60 65

DOMAIN 747 750

DOMAIN 1196 1220

DOMAIN 1196 1220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR00343; ABC_transportr.
InterPro; IPR003405; SMC_C.
InterPro; IPR003395; SMC_N.
Pfam; PF02443; SMC_C; 1.
Pfam; PF02463; SMC_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MITOTIC CHROMOSOMES:

-:- SUBURNIT: ASSOCIATES WITH XCAP-E PROBABLY AS HETERODIMER.
-:- SUBCELLULAR LOCATION: NUCLEAR. DURING CHROMOSOME ASSEMBLY IN MITOTIC EXTRACTS, XCAP-C/E WAS RECRUITED TO THE CHROMATIN AND FORMED A DISCRETE INTERNAL STRUCTURE WITHIN ASSEMBLED CHROMOSOMES.
-!- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
-!- SIMILARITY: BELONGS TO THE SMC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as modified and this statement is not removed. U entitles requires a license agreement (See htt or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                condensation in vitro.";
Cell 79:449-458(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U13673; AAA64679.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95042742; PubMed=7954811;
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *A heterodimeric coiled-coil protein required
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                                                                                 511
                                                                                                          190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ween the Swiss Institute of Bioinfo
European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: REQUIRED FOR BOTH ASSEMBLY
                                                                                                                                                                                                                                                                                                 MVEKEKDALEGEKNKAIEFLTVENETFKKKNQLCQYYIHDLQKRSRDKEAQKEKIQEDTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a een the Swiss Institute of Bioinformatics and the EMBL
                                                                                LSQLNKAKEALNTASATLKERRAAIKELETKLPKDEGD
                                                                                                                                                                                                                                                                      AIID---TLRDTLEERNATVESLQNALNKAEMLCSTLKKQMKFLEQRQDETKQ-----
                                                                                                                                  EEKLKNVMDSLKKETQGLQEEKEVKEKELMEISKTVNEARSKMDVAQSELDIYLSRHNSA
                                                                                                                                                     -EQLAVYCVSLKKEYENLKEARKATGELADRLKKDLVSSRSKLKTLNTELD-------
                                                                                                                                                                                        TREKLKHSKSKVKKLQK----QLQKDKEKVDELKNVPANSQKIIAEETNKKDLLEKQKEKE
                                                                                                                                                                                                                  AREEAHRLKCKMKTMEQIELLLQSQRSEVEEMIRDMGVGQSAV-------
                                                                                                                                                                                                                                            DISEKSNTLLETMKEKNKALKDVEKQLNKI-----TKFIEENREKFTQLDLQDVD
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                          QAKLELRSAQ----KDLQSADQEI-TSLRKKSDD 218
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841
1196
1290
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               STANDARD;
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22.7%;
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Coiled
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COILED COIL (POT
POLY-PRO.
POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                         MW.
                                                                                                                                                                                                                                                                                                                                                                     Score 148.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                    ALA/ASP-RICH (DA-BOX).
W; 2931249924FE90F6 CRC64;
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               PRT;
                                                                                                                                                                                                                                                                                                                                                        Mismatches
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               1427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     There are no rest
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(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                 1290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome
                                                                                                                                                                                                                                                                                                                                                       83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    outstation
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Matches
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TISSUE-Peripheral blood monocytes;
MEDLINE-92289675; PubMed-1600942;
Bilbe G., Delabie J., Brueggen J., Richener
Cerletti N., Sorg C., Odink K., Tarcsay L.,
de Wolf-Peeters C., Shipman R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSN.
Homo sapiens (Human).
Homo sapiens (Human).
Thervota; Metazoa; Chordata; Metazoa; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Restin (Cytoplasmic linker protein 170 alpha-2) (CLIP-170) (Reed-
The control of the control of
                                                                                                                                                                                                            VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-92405160; PubMed-1356075;

MEDLINE-92405160; PubMed-1356075;

Pierre P., Scheel J., Rickard J.E., Kreis T.E.;

"CLIP-170 links endocytic vesicles to microtubules

Cell 70:887-900(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Restin: a novel intermediate filament-associated pexpressed in the Reed-Sternberg cells of Hodgkin's EMBO J. 11:2103-2113(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents
                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01302; CAP_GLY; SMART; SM00343; ZnF_C2HC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X64838; CAA46050.1; EMBL; M97501; AAA35693.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformathe European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced throu between the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOSKELETON.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- FUNCTION: SEEMS TO BE A INTERMEDIATE FILAMENT ASSOCIATED THAT LINKS ENDOCYTIC VESICLES TO MICROTUBULES.
-i- SUBCELLULAR LOCATION: CYTOPLASMIC, ASSOCIATED WITH THE
                                                                                                                                                                                                                                                                                                                                                                                                                             Cytoskeleton;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00845; CAP_GLY_1; PROSITE; PS50245; CAP_GLY_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MIM; 179838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; S22695; S22695
                                                                                                                                                                                                                                                                                  DOMAIN
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                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000938; InterPro; IPR001878;
  878
                                                                                                                  Local
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                                                                                                                                             Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICITYS: HIGHLY EXPRESSED IN THE RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 2 CAP-GLY DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF HODGKIN'S DISEASE.
                                              NKLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREK-----
NMLSSDLEKLRENLADMEAKFREKDEREEQLI-KAKEKLENDIAEIMKMSGDNSSQLTKM 936
                                                                                              l Similarity
54; Conserv
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Microtubules;
                                                                                                                                                                                                              1069
A; 160989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _C2HC; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAP-Gly.
Znf_CCHC
SLY; 2.
                                                                                                                  23
                                                                                                                  . 98;
                                                                                                                                                                                                         SER-RICH.
CAP-GLY 1.
SER-RICH.
CAP-GLY 2.
SER-RICH.
COILED COIL (POTENTIAL
CCHC-BOX.
MISSING (IN SHORT ISOF
MISSING (IN REF. 2).
D-> E (IN REF. 2).
D-> LOTENDE COIL (POTENTIAL
CCHC-BOX.)
                                                                                              38;
                                                                                                               Score 148.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                              Mismatches
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                                                                                                                                                                                                                                                          (IN SHORT ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.isb-sib.ch/announce/
                                                                                                                  . 26;
                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Alternative splicing
                                                                                                                                                                                                                                                                                                        (POTENTIAL).
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THE RE
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Wiesendanger
                                                                                            87;
                                                                                                                                        1;
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LICING.
E REED-STERNBERG (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Asselbergs F.A.M., sendanger W.,
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s disease.";
                                                                                                                                                                                                              CRC64;
                                                                                            Indels
                                                                                                                                        Length
                                              ----RDSQAIIDTL
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RESULF RE
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MYH7_MESAU STANDARD
P13540; Q60540;
01-JAN-1990 (Rel. 13, C
15-JUL-1998 (Rel. 36, L
16-OCT-2001 (Rel. 40, L
                                                                                        EMBL; L12104; AAA62313.1;
EMBL; X07273; CAA30256.1;
PIR; A28298; A28298.
HSSP; P08799; 1MMD.
                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                  use
                                                                                                                                                                                                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wang R., Sole M.J., Cukerman E., Liew C.-C.; "Characterization and nucleotide sequence of heavy chain gene from Syrian hamster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=F1B; TISSUE=Liver; MEDLINE=95115033; PubMed=7815459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mesocricetus auratus (Golden hamster).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mesocricetus.
NCBI_TaxID=10036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myosin heavy
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                              InterPro;
                                                             InterPro; IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic Acids Res. 16:4737-4737(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heavy chain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Sequence of cDNA encoding the Syrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-88247788; PubMed-3380703;
Jandreski M.A., Sole M.J., Liew C.-C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 962-1935 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERISTIC FOR ALPHA-HELICAL COILED COILS.

MISCELLANEOUS: EACH MYOSIN HEAVY CHAIN CAN BE SPLIT INTO 1 LIGHT MEROMYOSIN (LMM) AND 1 HEAVY MEROMYOSIN (HMM). IT CAN LATER BE SPLIT FURTHER INTO 2 GLOBULAR SUBFRAGMENTS (S1) AND 1 ROD-SHAPED SUBFRAGMENT (S1).

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 IQ DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: MUSCLE CONTRACTION.

SUBUNIT: MUSCLE MYOSIN IS A HEXAMERIC PROTEIN THAT CONSISTS OF 2

HEAVY CHAIN SUBUNITS (MHC), 2 ALKALI LIGHT CHAIN SUBUNITS (MLC)

AND 2 REGULATORY LIGHT CHAIN SUBUNITS (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: THE RODLIKE TAIL SEQUENCE IS HIGHLY REPETITIVE, SHOWING

CYCLES OF A 28-RESIDUE REPEAT PATTERN COMPOSED OF 4 HEPTAPEPTIDES,
                                                                                                                                                                                                                                                                                                                                                       European Bioinformatics Institute.
                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way fied and this statement is not removed. Usage by and for commercial ties requires a license agreement (See http://www.isb-sib.ch/announce/
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   IPR004009;
IPR002928;
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                              Myosin_N.
Myosin_tail.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update 
Last annotation update
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beta isofo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hamster cardiac beta-myosin
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; Cricetinae;
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Best Local
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Pfam; PF01736; Myosin_N; 1.
Pfam; PF01576; Myosin_tail; 1.
PFRNTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM00012; MYSC; 1.
                                       1230
                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                     CONFLICT
1287 SRQLDEKEALISQLTRGKLTYTQQLEDLKRQLEE 1320
                                                                             1170
                                                                                                                   1110
                                                                                                                                                     1053 KLEGDLKLTQESIMDLENDKQQLDE---KLKKKDFELNALNARIEDEQALGSQLQKKLKE
                                                                                                                                                                                                                                                         CONFLICT
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MOD_RES
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Pfam; PF00612; IQ; 2.
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                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS50096; IQ; 1.
                                                          132
                                                                                               94
                                                                                                                                      59
                                                                                                                                                                            6
                   NTELDQAKLELRSAQKDLQSADQEITSLRKKSDD
                                                                                                                   LQARIEELEEELEAERTARAKVEKLRSDLSRELEEISERLEEAGGATSVQIEMNKKREAE 1169
                                                                                                                                     RNATVESLQNALN------KAEMLCSTLKKQMKFLEQRQDE--------
                                                                                                                                                                           KLFFDLAQEEENVLDAEFLKNELDSVKAQLSQKDREK-----RDSQAIIDTLRDTLEE
                                       V---TSNMEQIIKAKANLEKMCRTLEDQMNEHRSKAEETQRSVNDLTSQRAKLQTENGEL
                                                        MGVGQSAVEQLAVYCVSLKKEYENLKE----ARKATGELADRLKKDLVSSRSKLKT----L
                                                                           FQKMRRDLEEATLQHEATAAALRKKHADSVAELGEQIDNLQRVKQKLEKEKSEFKLELDD
                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein;
                                                                                              -TKQAREEAHRLKCK-------MKTMEQIELLLQSQRSEVEEMIRD
                                                                                                                                                                                                                                               ₽,
                                                                                                                                                                                                                                             779 MYC
809 IO
1944 ATI
184 ATI
676 ACI
770 ACI
128 MEE
1014 ALM
704 ALM
704 ALM
704 ALM
706 D
1057 D
1057 D
1057 D
1158 D
1157 D
1157 D
1157 D
1157 D
1158 C
1158 C
1159 MW:
                                                                                                                                                                                                        13.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Coiled coil; Thick filament; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alkylation; Multigene family;
                                                                                                                                                                                                56;
                                                                                                                                                                                                                                                        E -> Q (IN REF. 2).

DLQAEED -> ALEARKT (IN R D-> Y (IN REF. 2).

L -> V (IN REF. 2).

D -> N (IN REF. 2).

D -> N (IN REF. 2).

D -> N (IN REF. 2).

C -> R (IN REF. 2).

C -> R (IN REF. 2).

L -> V (IN REF. 2).

N -> K (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                ALKILOLIC (IN REF. 2).
D -> E (IN REF. 2).
T -> TE (IN REF. 2).
                                                                                                                                                                                                        Score 148.5; D
Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                            METHYLATION (TRI-)
ALKYLATION (SH-1)
ALKYLATION (SH-2)
                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIN-BINDING
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                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                              91;
                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                 Length 1934;
                                                                                                                                                                                                Indels
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                                                                                                                                                                                              67;
                                                                                                                                                                                              Gaps
                                                                                                                                                         1109
                                       1286
                                                                           1229
                                                                                               131
                                                                                                                                                                           58
                                                          184
                                                                                                                                      93
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